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Remarks:

The complete document including Reference Tables and the Sequence Listing is available on CD-ROM from the European Patent Office, Vienna sub-office

(54) **Full-length cDNA sequences**

(57) Novel full-length cDNAs are provided.
1970 cDNA derived from human have been isolated. The full-length nucleotide sequences of the cDNA and amino acid sequences encoded by the nucleotide

sequences have been determined. Because the cDNA of the present invention are full-length and contain the translation start site, they provide information useful for analyzing the functions of the polypeptide.

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Description**FIELD OF THE INVENTION**

5 **[0001]** The present invention relates to polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and new uses of these.

BACKGROUND OF THE INVENTION

10 **[0002]** Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 40 species of prokaryotes, a lower eukaryote, yeast, a multicellular eukaryote, *C. elegans*, and a higher plants, *arabidopsis*, etc. are already determined. For human genome, presumably having 3 billion base pairs, the analysis was advanced under global cooperative organization, and a draft sequence was disclosed in 2001. Moreover, all the structures are to be clear and
15 to be disclosed in 2002 - 2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academic subject, but also socially significant from the viewpoint of industrial application.

20 **[0003]** However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. On the other hand, the human genome has been estimated to contain about 30,000-40,000 genes. Further, 100,000 or more types of mRNAs are said to exist when variants produced by alternative splicing are taken into consideration. Therefore, it is desirable to establish "a high throughput analysis system of the
25 gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify
30 the primary structure of the protein easily. In human cDNA research, to date, more than three million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exon-regions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among human
35 cDNAs, the number of the corresponding mRNAs whose encoding full-length protein sequences are deduced is approximately 13,000.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains atg codon, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce
40 a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

45 **[0007]** Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

[0008] In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-related proteins (protein kinases, etc.), glycoprotein-related proteins, transcription-related proteins, etc.
50 are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-related proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0009] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired
55 since the protein itself would be useful as a medicine, and also the clones potentially include a gene involved in diseases. In addition, genes encoding proteins that are involved in signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly involved in diseases. Thus, identification of the full-length cDNA clones encoding those

proteins has great significance.

SUMMARY OF THE INVENTION

5 **[0010]** An objective of the present invention is to provide polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning, from a cDNA library having very high fullness-ratio, a human full-length cDNA that is predicted to be a full-length cDNA clone, where the cDNA library is synthesized by an improved method (WO 01/04286) of the oligo-capping method (K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)). Then, the nucleotide sequences of cDNA clones whose fullness ratio is high, obtained by this method, were determined mainly from their 5'-ends, and, if required, from 3'-ends.

10 **[0012]** Further, representative clones, which were estimated to be novel and full-length, among the clones obtained, were analyzed for their full-length nucleotide sequences. The determined full-length nucleotide sequences were analyzed by BLAST homology search of the databases shown below. Because the homology search of the present invention is carried out based on the information of full-length cDNAs including the entire coding regions, homology to every part of a polypeptide can be analyzed. Thus, in the present invention, the reliability of homology search has been greatly improved.

20 [1] SwissProt
(http://www.ebi.ac.uk/ebi_docs/SwissProt_db/swisshome.html),
[2] GenBank (<http://www.ncbi.nlm.nih.gov/web/GenBank>),
[3] UniGene (Human) (<http://www.ncbi.nlm.nih.gov/UniGene>), and
[4] nr (a protein database, which has been constructed by combining data of coding sequences (CDS) in nucleotide sequences deposited in GenBank, and data of SwissProt, PDB (<http://www.rcsb.org/pdb/index.html>), PIR (<http://pir.georgetown.edu/pirwww/pirhome.shtml>), and PRF (<http://www.prf.or.jp/en/>); overlapping sequences have been removed.)

30 **[0013]** Further, the gene expression profiles of cDNA clones whose full-length nucleotide sequence had been determined were studied by analyzing the large-scale cDNA database constructed based on the 5'-end nucleotide sequences of cDNAs obtained. In addition to the analysis for the expression profile by computer, the profiles of gene expression in living cells were also determined by PCR. The present inventors revealed the usefulness of the genes of the present invention based on these analysis results.

35 **[0014]** In the present invention, gene functions were revealed by the analysis of expression profiles *in silico* based on the information of full-length nucleotide sequences. The expression profiles used in the expression frequency analysis were studied based on the database containing sufficient amount of fragment sequence data. The expression frequency analysis was carried out by referring, for these expression profiles, to the full-length nucleotide sequences of many cDNA clones obtained in the present invention. Thus, a highly reliable analysis can be achieved by referring to the full-length nucleotide sequences of a wide variety of genes for the sufficiently large population for analysis (expression profiles). Namely, the results of expression frequency analysis using the full-length sequences of the present invention more precisely reflect the gene expression frequency in tissues and cells from which a certain cDNA library was derived. In other words, the information of full-length cDNA nucleotide sequence of the present invention made it possible to achieve the highly reliable expression frequency analysis.

40 **[0015]** The full-length cDNA clones of this invention were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the high fullness ratio by oligo-capping, and [2] assembling 5'-end sequences and selecting one with the highest probability of completeness in length- in the cluster formed (there are many clones longer in the 5'-end direction). However, the uses of primers designed based on the 5'- and 3'-end sequences of polynucleotides provided by the present invention enable readily obtaining full-length cDNAs without such a special technique. The primer, which is designed to be used for obtaining cDNAs capable of being expressed, is not limited to the 5'- and 3'-end sequences of polynucleotide.

50 **[0016]** Specifically, the present invention relates to a polynucleotide selected from the group consisting of the following (a) to (g):

- (a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs shown in Table 1;
- 55 (b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1;
- (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1, wherein, in said amino acid sequence, one or more amino

acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;

(d) a polynucleotide hybridizing under stringent conditions to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs shown in Table 1, wherein said nucleotide sequence encodes a polypeptide functionally

equivalent to a polypeptide encoded by the selected nucleotide sequence;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of (a); and

(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of (a).

[0017] The present invention also relates to a polypeptide encoded by the above-mentioned polynucleotide or a partial peptide thereof, an antibody binding to the polypeptide or the peptide, and a method for immunologically assaying the polypeptide or the peptide, which comprises the steps of contacting the polypeptide or the peptide with the antibody, and observing the binding between the two.

[0018] Furthermore, the present invention features a vector comprising the above-mentioned polynucleotide, a transformant carrying the polynucleotide or the vector, a transformant carrying the polynucleotide or the vector in an expressible manner, and a method for producing the polypeptide or the peptide, which comprises the steps of culturing the transformant and recovering an expression product.

[0019] Another feature of the present invention is an oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970 or to a complementary strand thereof. This oligonucleotide can be used as a primer for synthesizing the above-mentioned polynucleotide or used as a probe for detecting the polynucleotide. The present invention includes an antisense polynucleotide against the polynucleotide or a part thereof, and a method for detecting the polynucleotide, which comprises the following steps of:

- a) incubating a target polynucleotide with the oligonucleotide under hybridizable conditions, and
- b) detecting hybridization of the target polynucleotide with the oligonucleotide.

[0020] Still another feature of the present invention is a database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 1970 and/or on at least one of the amino acid sequences of SEQ ID NOs: 1971 to 3940.

[0021] Herein, "polynucleotide" is defined as a molecule, such as DNA and RNA, in which multiple nucleotides are polymerized. There are no limitations on the number of the polymerized nucleotides. In case that the polymer contains relatively low number of nucleotides, it is also described as an "oligonucleotide", which is included in the "polynucleotide" of the present invention. The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template polynucleotide by an enzymatic reaction such as PCR. Furthermore, the polynucleotide of the present invention may be modified chemically. Moreover, not only a single-strand polynucleotide but also a double-strand polynucleotide is included in the present invention. In this specification, especially in claims, when the polynucleotide is described merely as "polynucleotide", it means not only a single-strand polynucleotide but also a double-strand polynucleotide. When it means double-strand polynucleotide, the nucleotide sequence of only one chain is indicated. However, based on the nucleotide sequence of a sense chain, the nucleotide sequence of the complementary strand thereof is essentially determined.

[0022] As used herein, an "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring polynucleotide or to that of any fragment of a naturally occurring genomic polynucleotide spanning more than three separate genes. The term therefore includes, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule in the genome of the organism in which it naturally occurs; (b) a polynucleotide incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion polypeptide. Specifically excluded from this definition are polynucleotides of DNA molecules present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones; e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0023] The term "substantially pure" as used herein in reference to a given protein or polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. For example, the substantially pure protein or polypeptide is at least 75%, 80%, 85%, 95%, or 99% pure by dry weight. Purity can be measured by any

appropriate standard method known in the art, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0024] All the cDNAs provided by the present invention are full-length cDNAs. The "full-length cDNA" herein means that the cDNA contains the ATG codon, which is the start point of translation therein. The untranslated regions upstream and downstream of the protein-coding region, both of which are naturally contained in natural mRNAs, are not indispensable. It is preferable that the full-length cDNAs of the present invention contain the stop codon.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025]

Figure 1 shows the restriction map of the vector pME18SFL3.

DETAILED DESCRIPTION OF THE INVENTION

[0026] All the clones (1970 clones) of the present invention are novel and encode the full-length polypeptides. Further, all the clones are cDNAs with the high fullness ratio, which were obtained by oligo-capping method, and also clones which are not identical to any of known human mRNAs (namely, novel clones) selected by searching, for the 5'-end sequences, mRNA sequences with the annotation of "complete cds" in the GenBank and UniGene databases by using the BLAST homology search [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]; they are also clones that were assumed to have higher fullness ratio among the members in the cluster formed by assembling. Most of the clones assessed to have high fullness ratio in the cluster had the nucleotide sequences longer in the 5'-end direction.

[0027] All the full-length cDNAs of the present invention can be synthesized by a method such as PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) using primer sets designed based on the 5'-end and 3'-end sequences or using primer sets of primers designed based on the 5'-end sequences and a primer of oligo dT sequence corresponding to poly A sequence. Table 1 contains the clone names of full-length cDNA of 1970 clones of the present invention, SEQ ID NOs of the full-length nucleotide sequences, CDS portions deduced from the full-length nucleotide sequences, and SEQ ID NOs of the translated amino acids. The positions of CDS are shown according to the rule of "DDBJ/EMBL/GenBank Feature Table Definition" (<http://www.ncbi.nlm.nih.gov/colab/FT/index.html>). The start position number corresponds to the first letter of "ATG" that is the nucleotide triplet encoding methionine; the termination position number corresponds to the third letter of the stop codon. These are indicated being flanked with the mark "...". However, with respect to the clones having no stop codon, the termination position is indicated by the mark ">" according to the above rule.

Table 1

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
ADRGL20020290	1	62..1669	1971
ADRGL20021910	2	150..707	1972
ADRGL20022600	3	464..814	1973
ADRGL20023920	4	375..1853	1974
ADRGL20026790	5	113..2371	1975
ADRGL20027530	6	2013..2372	1976
ADRGL20036380	7	1129..1557	1977
ADRGL20036840	8	260..889	1978
ADRGL20040310	9	539..844	1979
ADRGL20040770	10	817..1227	1980
ADRGL20046760	11	1108..1467	1981
ADRGL20047080	12	823..1134	1982
ADRGL20047770	13	1532..1897	1983
ADRGL20057560	14	376..846	1984
ADRGL20059610	15	969..1961	1985
ADRGL20062330	16	799..>2117	1986
ADRGL20063770	17	344..664	1987

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	ADRGL20066770	18	22..1416	1988
	ADRGL20067320	19	276..1016	1989
	ADRGL20079060	20	63..1748	1990
	ADRGL20095330	21	929..1516	1991
	ASTR020001910	22	1753..>2216	1992
10	ASTR020003720	23	2089..2586	1993
	ASTR020004820	24	444..1040	1994
	ASTR020006530	25	2..1123	1995
	ASTR020009140	26	344..1714	1996
15	ASTR020010010	27	1236..1727	1997
	ASTR020010290	28	2..745	1998
	ASTR020012270	29	286..627	1999
	ASTR020020240	30	12..335	2000
	ASTR020020350	31	1384..1854	2001
20	ASTR020022020	32	467..1093	2002
	ASTR020026320	33	473..2161	2003
	ASTR020027330	34	481..1101	2004
	ASTR020038400	35	52..2025	2005
25	ASTR020045840	36	263..1051	2006
	ASTR020046280	37	140..1402	2007
	ASTR020047510	38	1240..1611	2008
	ASTR020050810	39	171..1694	2009
	ASTR020052420	40	1166..2362	2010
30	ASTR020053430	41	218..1885	2011
	ASTR020055530	42	209..559	2012
	ASTR020055570	43	242..733	2013
	ASTR020055930	44	343..1086	2014
35	ASTR020058960	45	55..1215	2015
	ASTR020069200	46	71..1237	2016
	ASTR020075150	47	1004..1795	2017
	ASTR020076660	48	1594..1968	2018
	ASTR020085080	49	470..2011	2019
40	ASTR020088950	50	346..1530	2020
	ASTR020089600	51	142..1125	2021
	ASTR020090680	52	1221..>2631	2022
	ASTR020091180	53	12..1214	2023
	ASTR020091770	54	10..318	2024
45	ASTR020141740	55	30..347	2025
	BGGI120000670	56	240..614	2026
	BGGI120010750	57	72..>2507	2027
	BNGH410000570	58	957..2027	2028
50	BNGH420008150	59	596..1606	2029
	BNGH420014060	60	1072..1413	2030
	BNGH420015760	61	92..1336	2031
	BNGH420021680	62	147..2093	2032
	BNGH420023870	63	301..1851	2033
55	BNGH420024870	64	155..1960	2034
	BNGH420035290	65	114..2126	2035
	BNGH420036410	66	1778..2143	2036

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BNGH420040760	67	698..1162	2037
	BNGH420042910	68	191..721	2038
	BNGH420045380	69	721..1254	2039
	BNGH420046790	70	1079..1429	2040
	BNGH420052350	71	787..1146	2041
10	BNGH420059680	72	213..2393	2042
	BNGH420061350	73	600..3131	2043
	BNGH420062340	74	294..641	2044
	BNGH420070370	75	567..2429	2045
15	BNGH420074600	76	125..1696	2046
	BNGH420075940	77	31..510	2047
	BNGH42007798	78	288..2147	2048
	BNGH420085100	79	243..569	2049
	BNGH420086030	80	107..>2556	2050
20	BNGH420087430	81	195..1835	2051
	BRACE10000510	82	642..1703	2052
	BRACE20003310	83	1379..2893	2053
	BRACE20007330	84	339..2015	2054
25	BRACE20009050	85	1023..1493	2055
	BRACE20014450	86	161..1096	2056
	BRACE20017790	87	304..639	2057
	BRACE20018810	88	397..1146	2058
	BRACE20025820	89	453..767	2059
30	BRACE20038920	90	1122..1463	2060
	BRACE20050870	91	110..1987	2061
	BRACE20051600	92	443..895	2062
	BRACE20051930	93	173..901	2063
35	BRACE20052430	94	825..1637	2064
	BRACE20052530	95	98..490	2065
	BRACE20054080	96	762..1382	2066
	BRACE20054480	97	111..902	2067
	BRACE20054600	98	392..1276	2068
40	BRACE20055560	99	136..735	2069
	BRACE20057870	100	1169..1825	2070
	BRACE20059110	101	1452..1910	2071
	BRACE20059810	102	689..2218	2072
45	BRACE20061620	103	162..1163	2073
	BRACE20062580	104	1164..1859	2074
	BRACE20063540	105	378..1670	2075
	BRACE20065470	106	427..1101	2076
	BRACE20066360	107	233..736	2077
50	BRACE20068710	108	1099..1440	2078
	BRACE20069000	109	1355..2305	2079
	BRACE20069110	110	576..917	2080
	BRACE20069440	111	278..1504	2081
55	BRACE20079200	112	928..1413	2082
	BRACE20079370	113	158..1522	2083
	BRACE20097540	114	1474..2103	2084
	BRACE20098860	115	693..1193	2085

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRACE20099070	116	53..1441	2086
	BRACE20194670	117	11..616	2087
	BRACE20196180	118	35..916	2088
	BRACE20196960	119	1454..1912	2089
	BRACE20200770	120	306..683	2090
10	BRACE20200970	121	426..764	2091
	BRACE20204670	122	760..2124	2092
	BRACE20205840	123	40..387	2093
	BRACE20207420	124	119..469	2094
15	BRACE20212450	125	168..590	2095
	BRACE20215410	126	111..1361	2096
	BRACE20216700	127	1403..1738	2097
	BRACE20216950	128	911..1315	2098
	BRACE20219360	129	198..596	2099
20	BRAMY10000980	130	254..616	2100
	BRAMY10001730	131	796..1158	2101
	BRAMY20000210	132	134..445	2102
	BRAMY20000250	133	190..1932	2103
25	BRAMY20001510	134	129..917	2104
	BRAMY20003540	135	144..2477	2105
	BRAMY20003880	136	191..808	2106
	BRAMY20005080	137	1638..1958	2107
30	BRAMY20013670	138	551..2881	2108
	BRAMY20016780	139	273..1985	2109
	BRAMY20020440	140	359..685	2110
	BRAMY20021580	141	67..555	2111
	BRAMY20023390	142	1568..1939	2112
35	BRAMY20023640	143	1684..2280	2113
	BRAMY20024790	144	276..626	2114
	BRAMY20027390	145	420..782	2115
	BRAMY20027990	146	529..1572	2116
	BRAMY20028530	147	973..1278	2117
40	BRAMY20028620	148	1048..1434	2118
	BRAMY20035380	149	925..1707	2119
	BRAMY20035830	150	219..977	2120
	BRAMY20036530	151	1411..1761	2121
45	BRAMY20036810	152	321..644	2122
	BRAMY20038980	153	715..>2057	2123
	BRAMY20039290	154	81..1043	2124
	BRAMY20040580	155	374..769	2125
	BRAMY20043520	156	942..1778	2126
50	BRAMY20043630	157	25..1119	2127
	BRAMY20044920	158	40..1947	2128
	BRAMY20045210	159	367..750	2129
	BRAMY20045420	160	4..888	2130
55	BRAMY20047560	161	220..726	2131
	BRAMY20050640	162	1802..2635	2132
	BRAMY20050940	163	23..385	2133
	BRAMY20051820	164	1411..2157	2134

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRAMY20052440	165	29..448	2135
	BRAMY20053910	166	11..358	2136
	BRAMY20055760	167	664..2253	2137
	BRAMY20056620	168	46..726	2138
	BRAMY20056840	169	40..1392	2139
10	BRAMY20063750	170	535..2166	2140
	BRAMY20072440	171	823..1620	2141
	BRAMY20072870	172	437..910	2142
	BRAMY20073080	173	3..353	2143
15	BRAMY20074110	174	314..838	2144
	BRAMY20074860	175	1135..1524	2145
	BRAMY20076100	176	459..1019	2146
	BRAMY20076130	177	59..376	2147
	BRAMY20076530	178	1010..1465	2148
20	BRAMY20083330	179	10..492	2149
	BRAMY20083820	180	625..1113	2150
	BRAMY20089770	181	173..955	2151
	BRAMY20091230	182	818..1579	2152
25	BRAMY20093490	183	637..1080	2153
	BRAMY20094890	184	30..2138	2154
	BRAMY20095080	185	239..613	2155
	BRAMY20095570	186	109..807	2156
	BRAMY20096930	187	1381..1800	2157
30	BRAMY20100680	188	268..870	2158
	BRAMY20102900	189	200..760	2159
	BRAMY20107980	190	343..669	2160
	BRAMY20111780	191	584..2209	2161
35	BRAMY20117670	192	63..782	2162
	BRAMY20118410	193	24..782	2163
	BRAMY20118490	194	39..791	2164
	BRAMY20120170	195	1130..1459	2165
	BRAMY20123400	196	1420..1755	2166
40	BRAMY20124970	197	825..1226	2167
	BRAMY20125170	198	157..579	2168
	BRAMY20125360	199	134..1060	2169
	BRAMY20125550	200	29..1747	2170
45	BRAMY20126910	201	114..518	2171
	BRAMY20127310	202	1986..2336	2172
	BRAMY20127760	203	317..691	2173
	BRAMY20134050	204	199..522	2174
	BRAMY20135720	205	57..401	2175
50	BRAMY20137360	206	976..2193	2176
	BRAMY20139440	207	2..1597	2177
	BRAMY20139750	208	88..435	2178
	BRAMY20143870	209	1419..2102	2179
55	BRAMY20152510	210	296..1993	2180
	BRAMY20155500	211	722..1069	2181
	BRAMY20158550	212	142..951	2182
	BRAMY20159250	213	286..810	2183

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRAMY20160020	214	143..919	2184
	BRAMY20173480	215	1544..1906	2185
	BRAMY20190550	216	114..1640	2186
	BRAMY20194680	217	1179..1517	2187
	BRAMY20204270	218	218..844	2188
10	BRAMY20206340	219	237..1805	2189
	BRAMY20219620	220	1014..1670	2190
	BRAMY20221600	221	168..992	2191
	BRAMY20223010	222	466..1257	2192
15	BRAMY20225250	223	368..673	2193
	BRAMY20225320	224	241..840	2194
	BRAMY20227230	225	1327..2067	2195
	BRAMY20227860	226	10..657	2196
	BRAMY20227960	227	1148..1558	2197
20	BRAMY20231150	228	199..1146	2198
	BRAMY20234820	229	199..2079	2199
	BRAMY20237190	230	397..870	2200
	BRAMY20238630	231	303..1331	2201
25	BRAMY20243120	232	1756..2451	2202
	BRAMY20244490	233	257..982	2203
	BRAMY20245140	234	3..1295	2204
	BRAMY20245350	235	94..750	2205
	BRAMY20245760	236	35..1375	2206
30	BRAMY20251210	237	68..955	2207
	BRAMY20251750	238	97..846	2208
	BRAMY20263000	239	216..1553	2209
	BRAMY20267780	240	1194..1706	2210
35	BRAMY20269040	241	989..2071	2211
	BRAMY20271140	242	1582..2238	2212
	BRAMY20274510	243	1785..2138	2213
	BRAMY20285650	244	23..382	2214
	BRAMY20287400	245	1..456	2215
40	BRAWH20014590	246	125..856	2216
	BRAWH20020470	247	131..>2130	2217
	BRAWH20020600	248	402..722	2218
	BRAWH20021910	249	394..1803	2219
45	BRAWH20025490	250	1699..2106	2220
	BRAWH20026010	251	307..2034	2221
	BRAWH20027250	252	942..1499	2222
	BRAWH20030000	253	381..1286	2223
	BRAWH20039640	254	109..>2281	2224
50	BRAWH20040680	255	201..2291	2225
	BRAWH20047790	256	290..631	2226
	BRAWH20050740	257	512..>1907	2227
	BRAWH20055240	258	1339..1653	2228
55	BRAWH20055330	259	1507..1911	2229
	BRAWH20055780	260	354..953	2230
	BRAWH20058120	261	896..1501	2231
	BRAWH20063010	262	1839..2579	2232

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRAWH20078080	263	161..745	2233
	BRAWH20078620	264	99..470	2234
	BRAWH20080580	265	35..1000	2235
	BRAWH20082550	266	2191..2670	2236
	BRAWH20082920	267	1579..2124	2237
10	BRAWH20093040	268	1202..1855	2238
	BRAWH20093070	269	469..1569	2239
	BRAWH20094900	270	712..2166	2240
	BRAWH20095900	271	247..2178	2241
15	BRAWH20173790	272	634..1428	2242
	BRAWH20174330	273	2532..3272	2243
	BRAWH20175230	274	1119..1451	2244
	BRAWH20175340	275	88..504	2245
	BRAWH20176850	276	32..2203	2246
20	BRAWH20182670	277	2751..3059	2247
	BRAWH20183170	278	106..909	2248
	BRAWH20185260	279	204..1946	2249
	BRAWH20185270	280	15..869	2250
25	BRAWH20186010	281	886..1389	2251
	BRAWH20188750	282	21..824	2252
	BRAWH20190530	283	410..1024	2253
	BRAWH20190550	284	55..1533	2254
	BRAWH20191980	285	1426..2172	2255
30	BRCAN10000760	286	548..1885	2256
	BRCAN10001050	287	388..828	2257
	BRCAN10001680	288	519..998	2258
	BRCAN20001480	289	114..449	2259
35	BRCAN20004180	290	8..331	2260
	BRCAN20005230	291	63..590	2261
	BRCAN20005410	292	52..1335	2262
	BRCOC10000400	293	11..3664	2263
	BRCOC20000470	294	283..1851	2264
40	BRCOC20003600	295	163..1455	2265
	BRHIP10000720	296	4..312	2266
	BRHIP10001040	297	76..1317	2267
	BRHIP20000210	298	7..378	2268
	BRHIP20003590	299	618..1238	2269
45	BRHIP20005060	300	756..1178	2270
	BRSSN20001970	301	89..526	2271
	BRSSN20005610	302	174..>2375	2272
	BRSSN20005660	303	2089..>2535	2273
50	BRSSN20066440	304	248..1474	2274
	BRSSN20074640	305	257..985	2275
	BRSSN20091190	306	1214..2002	2276
	BRSSN20092440	307	4..396	2277
	BRSSN20093890	308	94..717	2278
55	CD34C20001750	309	10..840	2279
	CTONG10000090	310	2551..2991	2280
	CTONG20000340	311	856..1929	2281

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	CTONG20002790	312	373..708	2282
	CTONG20004110	313	74..3079	2283
	CTONG20004520	314	146..772	2284
	CTONG20007660	315	192..1448	2285
	CTONG20008190	316	1313..1789	2286
10	CTONG200084	317	1034..1849	2287
	CTONG20015240	318	134..874	2288
	CTONG20017490	319	346..2235	2289
	CTONG20020660	320	219..635	2290
15	CTONG20020950	321	24..3257	2291
	CTONG20027660	322	103..942	2292
	CTONG20029030	323	102..2492	2293
	CTONG20030280	324	219..2891	2294
	CTONG20031150	325	2175..2546	2295
20	CTONG20031890	326	8..1705	2296
	CTONG20032930	327	352..3102	2297
	CTONG20033500	328	1683..2018	2298
	CTONG20033610	329	404..>3203	2299
25	CTONG20033750	330	95..1999	2300
	CTONG20035240	331	234..2687	2301
	CTONG20036800	332	432..770	2302
	CTONG20036990	333	1568..2347	2303
	CTONG20039370	334	114..470	2304
30	CTONG20041150	335	406..1164	2305
	CTONG20041260	336	477..2276	2306
	CTONG20042640	337	6..2381	2307
	CTONG20044230	338	1199..3205	2308
35	CTONG20044870	339	17..2554	2309
	CTONG20045500	340	226..1950	2310
	CTONG20046690	341	385..840	2311
	CTONG20049480	342	216..>3268	2312
	CTONG20050490	343	428..859	2313
40	CTONG20051100	344	48..419	2314
	CTONG20051450	345	1239..1823	2315
	CTONG20052780	346	976..1656	2316
	CTONG20053990	347	2233..>2955	2317
45	CTONG20055670	348	2306..2620	2318
	CTONG20055850	349	506..1246	2319
	CTONG20056150	350	95..1150	2320
	CTONG20057750	351	2355..2849	2321
	CTONG20057950	352	3061..3420	2322
50	CTONG20059130	353	109..2613	2323
	CTONG20060040	354	204..2630	2324
	CTONG20061290	355	226..819	2325
	CTONG20062730	356	307..687	2326
55	CTONG20063770	357	108..3203	2327
	CTONG20063930	358	250..2700	2328
	CTONG20065240	359	1983..2333	2329
	CTONG20065680	360	2369..2797	2330

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	CTONG20066110	361	122..1972	2331
	CTONG20068360	362	1136..1876	2332
	CTONG20069320	363	843..1238	2333
	CTONG20069420	364	130..600	2334
	CTONG20070090	365	561..2960	2335
10	CTONG2007072	366	431..2677	2336
	CTONG20070780	367	2..2896	2337
	CTONG20070910	368	87..1397	2338
	CTONG20071040	369	16..1551	2339
15	CTONG20071680	370	189..>2419	2340
	CTONG20072930	371	193..2643	2341
	CTONG20073990	372	749..2428	2342
	CTONG20074000	373	81..3185	2343
	CTONG20074170	374	153..1211	2344
20	CTONG20074740	375	2754..>3085	2345
	CTONG20076230	376	2192..2560	2346
	CTONG20076810	377	909..2402	2347
	CTONG20077760	378	1517..2170	2348
25	CTONG20078340	379	100..2229	2349
	CTONG20079590	380	149..1066	2350
	CTONG20080140	381	159..686	2351
	CTONG20081840	382	586..897	2352
	CTONG20083430	383	159..1325	2353
30	CTONG20083980	384	106..1440	2354
	CTONG20084020	385	301..666	2355
	CTONG20084660	386	217..753	2356
	CTONG20085210	387	769..1878	2357
35	CTONG20133720	388	15..350	2358
	CTONG20165590	389	1721..2044	2359
	CTONG20165750	390	216..1955	2360
	CTONG20166580	391	320..1612	2361
	CTONG20167750	392	159..461	2362
40	CTONG20168240	393	491..856	2363
	CTONG20168460	394	569..871	2364
	CTONG20169040	395	139..894	2365
	CTONG20169530	396	1076..1399	2366
45	CTONG20170940	397	184..1569	2367
	CTONG20174290	398	96..1826	2368
	CTONG20174440	399	1246..1623	2369
	CTONG20174580	400	1..1023	2370
	CTONG20176040	401	147..737	2371
50	CTONG20179390	402	1423..1881	2372
	CTONG20179890	403	335..2344	2373
	CTONG20179980	404	1821..2210	2374
	CTONG20180620	405	1556..1915	2375
55	CTONG20180690	406	366..1442	2376
	CTONG20181350	407	1167..1607	2377
	CTONG20183430	408	319..2706	2378
	CTONG20183830	409	393..2687	2379

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	CTONG20184130	410	1970..2536	2380
	CTONG20184830	411	323..1204	2381
	CTONG20186140	412	21..443	2382
	CTONG20186290	413	2170..2811	2383
	CTONG20186370	414	156..1244	2384
10	CTONG20186520	415	211..2136	2385
	CTONG20186550	416	260..811	2386
	CTONG20188080	417	207..2774	2387
	CTONG20189000	418	174..1682	2388
15	CTONG20190290	419	220..2205	2389
	CTONG20190630	420	34..2082	2390
	DFNES20016470	421	288..851	2391
	DFNES20018000	422	40..1596	2392
	DFNES20025500	423	766..1134	2393
20	DFNES20028170	424	289..1734	2394
	DFNES20029660	425	356..2443	2395
	DFNES20032550	426	35..931	2396
	DFNES20043710	427	108..929	2397
25	DFNES20046840	428	786..1310	2398
	DFNES20055400	429	343..1584	2399
	DFNES20057660	430	25..795	2400
	DFNES20063460	431	26..406	2401
	DFNES20072990	432	62..1156	2402
30	DFNES20073320	433	377..1735	2403
	DFNES20076340	434	167..898	2404
	DFNES20080880	435	11..1669	2405
	DFNES20088810	436	171..548	2406
35	DFNES20094820	437	107..1807	2407
	FCBBF10000230	438	104..3247	2408
	FCBBF10002200	439	480..782	2409
	FCBBF10004760	440	578..1978	2410
	FCBBF20018680	441	177..1724	2411
40	FCBBF20020440	442	382..885	2412
	FCBBF20021110	443	158..517	2413
	FCBBF20023490	444	64..1779	2414
	FCBBF20028980	445	694..1014	2415
45	FCBBF20029280	446	1680..2021	2416
	FCBBF20032930	447	90..452	2417
	FCBBF20033360	448	315..2369	2418
	FCBBF20035430	449	196..726	2419
	FCBBF20035490	450	131..1387	2420
50	FCBBF20036360	451	16..366	2421
	FCBBF20038230	452	1468..1908	2422
	FCBBF20038950	453	648..992	2423
	FCBBF20041380	454	612..2174	2424
55	FCBBF20043730	455	45..>2063	2425
	FCBBF20054390	456	1367..1756	2426
	FCBBF20056580	457	82..>2394	2427
	FCBBF20059660	458	672..1226	2428

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FCBBF20061310	459	1582..1980	2429
	FCBBF20066340	460	116..1024	2430
	FCBBF20070800	461	968..1447	2431
	FCBBF20070950	462	50..>2299	2432
	FCBBF30000010	463	74..643	2433
10	FCBBF30001020	464	16..348	2434
	FCBBF30001100	465	341..>3125	2435
	FCBBF30001150	466	1209..1631	2436
	FCBBF30002270	467	319..927	2437
15	FCBBF30002280	468	113..4036	2438
	FCBBF30002330	469	6..611	2439
	FCBBF30003610	470	1015..2019	2440
	FCBBF30004340	471	120..1013	2441
	FCBBF30004730	472	368..1027	2442
20	FCBBF30005180	473	155..2734	2443
	FCBBF30005360	474	29..2710	2444
	FCBBF30005500	475	251..2494	2445
	FCBBF30019140	476	40..2979	2446
	FCBBF30019180	477	140..1669	2447
25	FCBBF300192	478	1214..2269	2448
	FCBBF30021900	479	63..1973	2449
	FCBBF30022680	480	1308..2480	2450
	FCBBF30026580	481	170..2725	2451
30	FCBBF30029250	482	52..4086	2452
	FCBBP30035570	483	217..>2468	2453
	FCBBF30042610	484	33..1244	2454
	FCBBF30048420	485	144..1094	2455
35	FCBBF30053300	486	62..2182	2456
	FCBBF30056980	487	1098..1415	2457
	FCBBF30062490	488	128..1063	2458
	FCBBF30063990	489	250..828	2459
	FCBBF30068210	490	51..2762	2460
40	FCBBF30071500	491	227..>2898	2461
	FCBBF30072440	492	2485..2865	2462
	FCBBF30072480	493	2602..>3057	2463
	FCBBF30074530	494	1031..1432	2464
	FCBBF30074620	495	840..1316	2465
45	FCBBF30075970	496	146..460	2466
	FCBBF30076310	497	42..1007	2467
	FCBBF30078600	498	113..1399	2468
	FCBBF30079770	499	693..2777	2469
50	FCBBF30080730	500	54..467	2470
	FCBBF30081000	501	526..924	2471
	FCBBF30085560	502	60..1919	2472
	FCBBF30088700	503	39..>3015	2473
	FCBBF30089380	504	8..2701	2474
55	FCBBF30091010	505	172..>3465	2475
	FCBBF30091520	506	56..2284	2476
	FCBBF30093170	507	974..1528	2477

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FCBBF30095410	508	64..1002	2478
	FCBBF30099490	509	2939..3256	2479
	FCBBF30100080	510	1237..1656	2480
	FCBBF30100120	511	8..2305	2481
	FCBBF30100410	512	121..1374	2482
10	FCBBF30101240	513	1696..2382	2483
	FCBBF30101300	514	3802..>4413	2484
	FCBBF30105080	515	973..1836	2485
	FCBBF30105440	516	1354..2040	2486
15	FCBBF30105860	517	355..>2524	2487
	FCBBF30106950	518	192..944	2488
	FCBBF30107290	519	1002..1610	2489
	FCBBF30107330	520	703..1071	2490
	FCBBF30114180	521	1777..2289	2491
20	FCBBF30114850	522	769..1503	2492
	FCBBF30115230	523	417..755	2493
	FCBBF30115920	524	543..1802	2494
	FCBBF30118670	525	891..2807	2495
25	FCBBF30118890	526	184..>2630	2496
	FCBBF30125460	527	67..1926	2497
	FCBBF30125880	528	185..670	2498
	FCBBF30128420	529	1789..2130	2499
	FCBBF30129010	530	184..1236	2500
30	FCBBF30130410	531	1149..1874	2501
	FCBBF30130580	532	156..2123	2502
	FCBBF30132050	533	718..1854	2503
	FCBBF30132660	534	86..1051	2504
35	FCBBF30135890	535	214..>2483	2505
	FCBBF30136230	536	24..3338	2506
	FCBBF30138000	537	646..2901	2507
	FCBBF30142290	538	679..1662	2508
	FCBBF30143550	539	111..3191	2509
40	FCBBF30145670	540	1533..1880	2510
	FCBBF30151190	541	974..1312	2511
	FCBBF30153170	542	16..2307	2512
	FCBBF30157270	543	84..>3303	2513
45	FCBBF30161780	544	21..659	2514
	FCBBF30164510	545	561..3035	2515
	FCBBF30166220	546	178..483	2516
	FCBBF30169280	547	116..901	2517
	FCBBF30169870	548	102..407	2518
50	FCBBF30170710	549	8..382	2519
	FCBBF30171230	550	1735..2361	2520
	FCBBF30172330	551	2497..2952	2521
	FCBBF30173960	552	106..>3530	2522
	FCBBF30175350	553	2..721	2523
55	FCBBF30177290	554	378..923	2524
	FCBBF30179180	555	2382..>3452	2525
	FCBBF30179740	556	299..721	2526

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FCBBF30181730	557	43..351	2527
	FCBBF30194370	558	698..1057	2528
	FCBBF30194550	559	9..1982	2529
	FCBBF30195690	560	15..1682	2530
	FCBBF30195700	561	14..376	2531
10	FCBBF30197840	562	406..3015	2532
	FCBBF30198670	563	421..2733	2533
	FCBBF30201630	564	1407..2561	2534
	FCBBF30212210	565	1669..2502	2535
15	FCBBF30215240	566	774..1586	2536
	FCBBF30220050	567	1431..2006	2537
	FCBBF30222910	568	117..614	2538
	FCBBF30223110	569	647..1129	2539
	FCBBF30223210	570	141..680	2540
20	FCBBF30225930	571	166..1956	2541
	FCBBF30228940	572	79..453	2542
	FCBBF30230610	573	99..440	2543
	FCBBF30236670	574	1889..2719	2544
25	FCBBF30250980	575	214..2514	2545
	FCBBF30255680	576	27..>2480	2546
	FCBBF3025737	577	2..1873	2547
	FCBBF30259050	578	104..1600	2548
	FCBBF30260210	579	115..>2494	2549
30	FCBBF30260480	580	28..519	2550
	FCBBF30263080	581	535..900	2551
	FCBBF30266510	582	445..3378	2552
	FCBBF30271990	583	187..1704	2553
35	FCBBF30275590	584	51..>2374	2554
	FCBBF30282020	585	123..1721	2555
	FCBBF30285930	586	260..697	2556
	FCBBF30287940	587	1636..2079	2557
	FCBBF40000610	588	586..1131	2558
40	FCBBF40001920	589	753..1082	2559
	FCBBF40005000	590	57..446	2560
	FCBBF50000410	591	930..1256	2561
	FCBBF50000610	592	383..697	2562
45	FCBBF50001650	593	562..1815	2563
	FCBBF50003530	594	127..921	2564
	FCBBF50004950	595	2156..2545	2565
	FEBRA20005040	596	295..2100	2566
	FEBRA20007820	597	160..690	2567
50	FEBRA20018670	598	184..1077	2568
	FEBRA20026820	599	103..1836	2569
	FEBRA20027070	600	663..1736	2570
	FEBRA20029620	601	565..1206	2571
55	FEBRA20031000	602	380..2551	2572
	FEBRA20031150	603	2925..3293	2573
	FEBRA20031280	604	362..3124	2574
	FEBRA20031810	605	1093..1455	2575

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FEBRA20035200	606	2607..3215	2576
	FEBRA20035240	607	74..826	2577
	FEBRA20038220	608	157..1305	2578
	FEBRA20038330	609	1612..2253	2579
	FEBRA20038970	610	1279..2811	2580
10	FEBRA20039070	611	967..1575	2581
	FEBRA20039260	612	23..685	2582
	FEBRA20040230	613	1663..2076	2583
	FEBRA20040260	614	244..561	2584
15	FEBRA20040290	615	1488..2330	2585
	FEBRA20040560	616	711..1496	2586
	FEBRA20045380	617	81..398	2587
	FEBRA20046200	618	125..2062	2588
	FEBRA20046280	619	694..1017	2589
20	FEBRA20046510	620	859..2256	2590
	FEBRA20057010	621	757..1107	2591
	FEBRA20063720	622	118..1878	2592
	FEBRA20076200	623	303..680	2593
25	FEBRA20078180	624	1517..1888	2594
	FEBRA20078800	625	24..644	2595
	FEBRA20080860	626	584..2419	2596
	FEBRA20082660	627	114..1793	2597
	FEBRA20083410	628	1169..1561	2598
30	FEBRA20084750	629	888..1202	2599
	FEBRA20086600	630	670..1407	2600
	FEBRA20087550	631	1140..1814	2601
	FEBRA20088610	632	315..818	2602
35	FEBRA20088810	633	1302..2021	2603
	FEBRA20090160	634	1..732	2604
	FEBRA20090220	635	106..2271	2605
	FEBRA20091620	636	1528..1935	2606
	FEBRA20092760	637	694..1317	2607
40	FEBRA20093270	638	2205..2507	2608
	FEBRA20093280	639	2165..2485	2609
	FEBRA20095410	640	267..647	2610
	FEBRA20098040	641	43..459	2611
45	FEBRA20099860	642	55..573	2612
	FEBRA20101410	643	396..740	2613
	FEBRA20108020	644	181..492	2614
	FEBRA20108580	645	542..901	2615
	FEBRA20115930	646	58..1494	2616
50	FEBRA20116650	647	178..573	2617
	FEBRA20121200	648	972..1490	2618
	FEBRA20121950	649	1217..1723	2619
	FEBRA20141980	650	644..955	2620
55	FEBRA20150420	651	314..3124	2621
	FEBRA20151750	652	52..>2299	2622
	FEBRA20163980	653	93..1223	2623
	FEBRA20170240	654	385..1632	2624

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FEBRA20172230	655	377..1363	2625
	FEBRA20173330	656	462..2378	2626
	FEBRA20175020	657	2040..2438	2627
	FEBRA20175330	658	62..520	2628
	FEBRA20177800	659	1918..2289	2629
10	FEBRA20180510	660	350..889	2630
	FEBRA20182030	661	341..745	2631
	FEBRA20187460	662	395..736	2632
	FEBRA20191720	663	417..836	2633
15	HCHON10000150	664	197..670	2634
	HCHON10001660	665	913..1338	2635
	HCHON20000870	666	442..1857	2636
	HCHON20002650	667	4..792	2637
	HCHON20002710	668	169..1437	2638
20	HCHON20015050	669	529..1995	2639
	HEART10001420	670	4..1476	2640
	HEART10001490	671	159..1121	2641
	HEART20009590	672	1369..1938	2642
25	HEART20019310	673	47..1693	2643
	HEART20022200	674	11..1378	2644
	HEART20031680	675	1033..3018	2645
	HEART20047640	676	595..2904	2646
	HEART20063100	677	131..826	2647
30	HEART20082570	678	18..1022	2648
	HHDPC10001140	679	506..1102	2649
	HHDPC20051850	680	21..422	2650
	HHDPC20081230	681	132..2195	2651
35	HHDPC20082790	682	150..608	2652
	HHDPC20082970	683	1445..1771	2653
	HHDPC20088160	684	214..>2639	2654
	HLUNG20008460	685	157..1818	2655
	HLUNG20009260	686	1035..1856	2656
40	HLUNG20009550	687	16..657	2657
	HLUNG20010130	688	1083..1400	2658
	HLUNG20011260	689	135..479	2659
	HLUNG20011440	690	803..1207	2660
	HLUNG20011460	691	43..1587	2661
45	HLUNG20012140	692	188..508	2662
	HLUNG20014590	693	1015..>2241	2663
	HLUNG20015070	694	377..1945	2664
	HLUNG20015180	695	468..1808	2665
50	HLUNG20020500	696	1232..1687	2666
	HLUNG20020850	697	802..1179	2667
	HLUNG20021450	698	753..1109	2668
	HLUNG20023030	699	2466..2855	2669
	HLUNG20024050	700	651..1568	2670
55	HLUNG20025620	701	1424..1765	2671
	HLUNG20028110	702	164..1996	2672
	HLUNG20029420	703	160..774	2673

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	HLUNG20029490	704	135..563	2674
	HLUNG20030420	705	116..1906	2675
	HLUNG20030490	706	553..1608	2676
	HLUNG20030610	707	920..1465	2677
	HLUNG20031620	708	604..1038	2678
10	HLUNG20032460	709	29..1582	2679
	HLUNG20033060	710	1085..>2287	2680
	HLUNG20033310	711	1319..1654	2681
	HLUNG20033350	712	1035..>2205	2682
15	HLUNG20034970	713	1046..1747	2683
	HLUNG20037140	714	1342..1698	2684
	HLUNG20037160	715	1704..3152	2685
	HLUNG20037780	716	1190..1855	2686
	HLUNG20038330	717	433..1284	2687
20	HLUNG20041540	718	199..1542	2688
	HLUNG20041590	719	130..>2341	2689
	HLUNG20042730	720	150..1484	2690
	HLUNG20045340	721	189..608	2691
25	HLUNG20047070	722	1310..1672	2692
	HLUNG20050760	723	1813..2118	2693
	HLUNG20051330	724	55..>2821	2694
	HLUNG20052300	725	88..1008	2695
	HLUNG20054790	726	1418..2548	2696
30	HLUNG20055240	727	204..554	2697
	HLUNG20056560	728	6..512	2698
	HLUNG20057380	729	303..788	2699
	HLUNG20059240	730	1529..1870	2700
35	HLUNG20060670	731	753..1517	2701
	HLUNG20063700	732	1356..1685	2702
	HLUNG20065700	733	90..911	2703
	HLUNG20065990	734	344..1231	2704
	HLUNG20067810	735	178..639	2705
40	HLUNG20068120	736	853..1281	2706
	HLUNG20069350	737	198..1871	2707
	HLUNG20070410	738	474..929	2708
	HLUNG20072100	739	164..1879	2709
45	HLUNG20072190	740	1394..1723	2710
	HLUNG20072450	741	127..468	2711
	HLUNG20074330	742	1621..>1976	2712
	HLUNG20079310	743	1484..2050	2713
	HLUNG200813	744	123..1910	2714
50	HLUNG20081530	745	1218..1889	2715
	HLUNG20082350	746	313..2109	2716
	HLUNG20083330	747	770..1138	2717
	HLUNG20083480	748	183..1895	2718
	HLUNG20083840	749	1389..1811	2719
55	HLUNG20083960	750	1214..1630	2720
	HLUNG20084790	751	1185..1745	2721
	HLUNG20085210	752	138..779	2722

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	HLUNG20088750	753	1321..1635	2723
	HLUNG20092530	754	224..577	2724
	HLUNG20093030	755	1836..2246	2725
	HLUNG20094130	756	2129..2554	2726
10	KIDNE20011600	757	197..601	2727
	KIDNE20016360	758	81..2798	2728
	KIDNE20024380	759	1017..>1994	2729
	KIDNE20027980	760	329..1891	2730
	KIDNE20080690	761	1..1500	2731
15	KIDNE20081170	762	1356..2444	2732
	KIDNE20083150	763	863..1342	2733
	KIDNE20083620	764	216..1142	2734
	KIDNE20084030	765	28..1572	2735
	KIDNE20084040	766	318..926	2736
20	KIDNE20084730	767	580..2511	2737
	KIDNE20084800	768	9..332	2738
	KIDNE20086490	769	162..1919	2739
	KIDNE20086660	770	341..700	2740
25	KIDNE20086970	771	202..846	2741
	KIDNE20087880	772	668..1003	2742
	KIDNE20088240	773	101..1135	2743
	KIDNE20089870	774	212..1621	2744
	KIDNE20091090	775	272..670	2745
30	KIDNE20094260	776	125..442	2746
	KIDNE20094670	777	997..2232	2747
	KIDNE20095530	778	1573..>1878	2748
	KIDNE20133460	779	210..>1556	2749
35	KIDNE20133880	780	743..1057	2750
	KIDNE20134130	781	174..797	2751
	KIDNE20134890	782	384..923	2752
	KIDNE20137310	783	304..876	2753
	KIDNE20138450	784	499..828	2754
40	KIDNE20140870	785	750..>3206	2755
	KIDNE20141120	786	1387..1932	2756
	KIDNE20141700	787	1825..2286	2757
	KIDNE20142680	788	796..1239	2758
45	KIDNE20142900	789	45..764	2759
	KIDNE20143200	790	982..1452	2760
	KIDNE20147170	791	1017..1493	2761
	KIDNE20148080	792	1097..1675	2762
	KIDNE20149780	793	267..1370	2763
50	KIDNE20150730	794	1671..1991	2764
	KIDNE20152440	795	3..1346	2765
	KIDNE20154330	796	422..2713	2766
	KIDNE20154830	797	1588..1923	2767
55	KIDNE20155980	798	1164..1595	2768
	KIDNE20157100	799	90..1286	2769
	KIDNE20160360	800	413..2692	2770
	KIDNE20160960	801	10..534	2771

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	KIDNE20163710	802	1605..1973	2772
	KIDNE20165390	803	68..2341	2773
	KIDNE20169180	804	125..2146	2774
	KIDNE20170400	805	597..2192	2775
	KIDNE20173150	806	51..1052	2776
10	KIDNE20173430	807	136..1296	2777
	KIDNE20176030	808	2418..2879	2778
	KIDNE20181670	809	180..659	2779
	KIDNE20182540	810	135..1745	2780
15	KIDNE20186170	811	83..748	2781
	KIDNE20188630	812	519..926	2782
	KIDNE20189890	813	1834..2445	2783
	KIDNE20189960	814	284..1666	2784
	KIDNE20191870	815	860..1372	2785
20	LIVER20006260	816	379..1668	2786
	LIVER20007690	817	329..760	2787
	LIVER20007750	818	176..1549	2788
	LIVER20010510	819	757..1143	2789
25	LIVER20010760	820	95..838	2790
	LIVER20010990	821	305..1009	2791
	LIVER20011640	822	1187..2086	2792
	LIVER20013890	823	1528..2199	2793
	LIVER20026440	824	1019..1963	2794
30	LIVER20030650	825	1469..2239	2795
	LIVER20032340	826	2181..2504	2796
	LIVER20038000	827	78..1004	2797
	LIVER20040740	828	195..1370	2798
35	LIVER20055270	829	148..1347	2799
	MESAN20006200	830	2690..3235	2800
	MESAN20007110	831	1401..1823	2801
	MESAN20008150	832	136..3567	2802
	MESAN20008940	833	122..514	2803
40	MESAN20009090	834	247..1992	2804
	MESAN20016270	835	346..2031	2805
	MESAN20021130	836	1540..2676	2806
	MESAN20021220	837	94..2322	2807
45	MESAN20021470	838	658..1446	2808
	MESAN20021860	839	217..1113	2809
	MESAN20026870	840	63..2450	2810
	MESAN20027240	841	39..1940	2811
	MESAN20027900	842	212..3322	2812
50	MESAN20029780	843	1900..2331	2813
	MESAN20030350	844	142..2239	2814
	MESAN20030370	845	735..2462	2815
	MESAN20030390	846	3..389	2816
55	MESAN20033220	847	68..478	2817
	MESAN20034440	848	42..2183	2818
	MESAN20038520	849	31..2547	2819
	MESAN20041380	850	7..342	2820

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	MESAN20045750	851	145..1002	2821
	MESAN20056890	852	187..1125	2822
	MESAN20057240	853	101..778	2823
	MESAN20058110	854	174..1022	2824
	MESAN20059570	855	280..1782	2825
10	MESAN20060220	856	464..775	2826
	MESAN20060430	857	1589..3469	2827
	MESAN20065990	858	213..533	2828
	MESAN20067430	859	1287..1973	2829
15	MESAN20069530	860	336..>3472	2830
	MESAN20084150	861	78..665	2831
	MESAN20085360	862	1168..1656	2832
	MESAN20089260	863	169..1254	2833
	MESAN20090190	864	256..2898	2834
20	MESAN20094180	865	1696..2139	2835
	MESAN20095220	866	1118..1972	2836
	MESAN20095800	867	31..1137	2837
	NESOP20004520	868	109..1512	2838
25	NESOP20005040	869	316..1308	2839
	NT2NE20013740	870	1413..1772	2840
	NT2NE20018890	871	39..1061	2841
	NT2NE20021860	872	268..1653	2842
	NT2NE20026200	873	1888..2907	2843
30	NT2NE20026510	874	338..1381	2844
	NT2NE20028700	875	166..1377	2845
	NT2NE20033150	876	496..912	2846
	NT2NE20037050	877	19..411	2847
35	NT2NE20038870	878	190..1548	2848
	NT2NE20039210	879	226..639	2849
	NT2NE20042550	880	708..1568	2850
	NT2NE20045190	881	33..599	2851
	NT2NE20047870	882	314..1207	2852
40	NT2NE20053230	883	622..1068	2853
	NT2NE20053950	884	133..993	2854
	NT2NE20059210	885	35..391	2855
	NT2NE20059680	886	120..443	2856
45	NT2NE20060750	887	239..928	2857
	NT2NE20061030	888	160..600	2858
	NT2NE20062880	889	201..539	2859
	NT2NE20064780	890	284..1771	2860
	NT2NE20066590	891	821..1204	2861
50	NT2NE20069580	892	1404..2282	2862
	NT2NE20070520	893	347..661	2863
	NT2NE20073650	894	756..1088	2864
	NT2NE20077250	895	1815..3185	2865
55	NT2NE20077270	896	250..>3642	2866
	NT2NE20077860	897	589..1053	2867
	NT2NE20079670	898	404..1867	2868
	NT2NE20080770	899	1181..1483	2869

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2NE20082130	900	1026..1457	2870
	NT2NE20082600	901	688..1227	2871
	NT2NE20086070	902	503..823	2872
	NT2NE20087270	903	276..1709	2873
	NT2NE20087850	904	9..326	2874
10	NT2NE20088030	905	682..1023	2875
	NT2NE20092950	906	142..1884	2876
	NT2NE20095230	907	547..1602	2877
	NT2NE20104000	908	217..702	2878
15	NT2NE20107810	909	29..376	2879
	NT2NE20108420	910	1135..>2525	2880
	NT2NE20111190	911	202..651	2881
	NT2NE20112210	912	963..2231	2882
	NT2NE20114850	913	1441..>1794	2883
20	NT2NE20117580	914	271..912	2884
	NT2NE20119980	915	445..843	2885
	NT2NE20123610	916	118..717	2886
	NT2NE20124570	917	1279..1620	2887
25	NT2NE20126030	918	1054..1548	2888
	NT2NE20127900	919	85..1599	2889
	NT2NE20140130	920	355..753	2890
	NT2NE20140280	921	126..989	2891
	NT2NE20141040	922	53..811	2892
30	NT2NE20145250	923	94..531	2893
	NT2NE20146510	924	125..661	2894
	NT2NE20148690	925	544..861	2895
	NT2NE20149500	926	454..888	2896
35	NT2NE20150610	927	73..432	2897
	NT2NE20152620	928	1080..2516	2898
	NT2NE20153620	929	133..1512	2899
	NT2NE20155650	930	716..1210	2900
	NT2NE20157120	931	927..1271	2901
40	NT2NE20165190	932	85..531	2902
	NT2NE20167660	933	20..349	2903
	NT2NE20173970	934	274..>2188	2904
	NT2NE20177210	935	115..675	2905
45	NT2NE20181760	936	201..785	2906
	NT2NE20181800	937	784..1137	2907
	NT2NE20184720	938	1033..1506	2908
	NT2RI20016240	939	359..748	2909
	NT2RI20021200	940	534..875	2910
50	NT2RI20033920	941	269..1444	2911
	NT2RI20093010	942	1478..1816	2912
	NT2RP70001120	943	172..1518	2913
	NT2RP70001730	944	166..1935	2914
55	NT2RP70003110	945	15..1868	2915
	NT2RP70012830	946	280..2337	2916
	NT2RP70022820	947	2819..>3760	2917
	NT2RP70027790	948	389..2965	2918

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2RP70029780	949	156..1349	2919
	NT2RP70030840	950	278..2983	2920
	NT2RP70031070	951	148..1740	2921
	NT2RP70031340	952	107..1576	2922
	NT2RP70031480	953	203..2947	2923
10	NT2RP70035110	954	106..765	2924
	NT2RP70046410	955	155..1582	2925
	NT2RP70049610	956	834..1889	2926
	NT2RP70056290	957	2748..3182	2927
15	NT2RP70056690	958	253..>3053	2928
	NT2RP70057500	959	216..2615	2929
	NT2RP70064570	960	636..2162	2930
	NT2RP70074800	961	199..684	2931
	NT2RP70075300	962	226..1539	2932
20	NT2RP70075800	963	211..3801	2933
	NT2RP70080150	964	306..674	2934
	NT2RP70084540	965	8..406	2935
	NT2RP70087140	966	175..1074	2936
25	NT2RP70090870	967	272..2617	2937
	NTONG20002230	968	50..>3211	2938
	NTONG20005310	969	88..471	2939
	NTONG20017620	970	40..432	2940
	NTONG20029850	971	110..1258	2941
30	NTONG20031580	972	126..863	2942
	NTONG20032100	973	65..1132	2943
	NTONG20034540	974	163..2523	2944
	NTONG20035150	975	543..2477	2945
35	NTONG20043080	976	22..2679	2946
	NTONG20048440	977	89..1849	2947
	NTONG20049180	978	155..1300	2948
	NTONG20053630	979	321..3821	2949
	NTONG20053730	980	121..1701	2950
40	NTONG20053910	981	47..2758	2951
	NTONG20055200	982	122..1969	2952
	NTONG20058010	983	237..1559	2953
	NTONG20058220	984	67..1314	2954
45	OCBBF20000740	985	165..2402	2955
	OCBBF20001780	986	1990..2334	2956
	OCBBF20005220	987	590..2299	2957
	OCBBF20009820	988	281..823	2958
	OCBBF20011860	989	145..528	2959
50	OCBBF20012520	990	786..3023	2960
	OCBBF20016390	991	667..1617	2961
	OCBBF20016810	992	123..2351	2962
	OCBBF20109450	993	204..506	2963
	OCBBF20109780	994	253..573	2964
55	OCBBF20110210	995	8..1072	2965
	OCBBF20110730	996	1346..1666	2966
	OCBBF20111370	997	296..1345	2967

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	OCBBF20111600	998	375..1823	2968
	OCBBF20112280	999	447..860	2969
	OCBBF20112320	1000	72..857	2970
	OCBBF20113110	1001	292..738	2971
	OCBBF20115360	1002	1182..2126	2972
10	OCBBF20116250	1003	124..2175	2973
	OCBBF20117220	1004	605..937	2974
	OCBBF20118720	1005	131..451	2975
	OCBBF20119810	1006	1483..2478	2976
15	OCBBF20120010	1007	216..1106	2977
	OCBBF20120950	1008	91..1629	2978
	OCBBF20121910	1009	235..2580	2979
	OCBBF20123200	1010	1046..1411	2980
	OCBBF20142290	1011	94..900	2981
20	OCBBF20147070	1012	1193..3256	2982
	OCBBF20152330	1013	284..613	2983
	OCBBF20155030	1014	188..724	2984
	OCBBF20156450	1015	104..1132	2985
25	OCBBF20157970	1016	1390..2313	2986
	OCBBF20160380	1017	1176..3884	2987
	OCBBF20165900	1018	407..934	2988
	OCBBF20165910	1019	1260..2495	2989
	OCBBF20166890	1020	201..1121	2990
30	OCBBF20166900	1021	350..>2606	2991
	OCBBF20167290	1022	186..2858	2992
	OCBBF20170350	1023	8..499	2993
	OCBBF20174580	1024	179..1294	2994
	OCBBF20174890	1025	178..1380	2995
35	OCBBF20175360	1026	1394..1711	2996
	OCBBF20176650	1027	121..423	2997
	OCBBF20177540	1028	334..1242	2998
	OCBBF20177910	1029	1047..1688	2999
40	OCBBF20182060	1030	964..1827	3000
	OCBBF20185630	1031	1839..2195	3001
	OCBBF20188280	1032	322..696	3002
	OCBBF20191950	1033	47..2305	3003
45	PANCR10000860	1034	20..376	3004
	PEBLM10001470	1035	155..1960	3005
	PEBLM20001800	1036	59..1549	3006
	PEBLM20003260	1037	660..1121	3007
	PEBLM20005020	1038	315..647	3008
50	PLACE50001290	1039	620..1030	3009
	PLACE50001390	1040	156..1376	3010
	PLACE60001910	1041	1521..2252	3011
	PLACE60004260	1042	562..924	3012
55	PLACE60006300	1043	12..725	3013
	PLACE60011180	1044	526..894	3014
	PLACE60012620	1045	106..1368	3015
	PLACE60017120	1046	1116..1454	3016

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	PLACE60052940	1047	385..>2108	3017
	PLACE60053280	1048	161..>2687	3018
	PLACE60054230	1049	189..1550	3019
	PLACE60054820	1050	298..852	3020
	PLACE60054870	1051	105..2213	3021
10	PLACE60055350	1052	1188..1562	3022
	PLACE60055460	1053	160..1197	3023
	PLACE60055590	1054	123..1406	3024
	PLACE60056910	1055	1028..1549	3025
15	PLACE60057860	1056	1617..1940	3026
	PLACE60061370	1057	1..1899	3027
	PLACE60062660	1058	97..954	3028
	PLACE60062870	1059	604..1278	3029
	PLACE60063940	1060	459..797	3030
20	PLACE60064180	1061	167..1240	3031
	PLACE60064740	1062	302..952	3032
	PLACE60066970	1063	697..1998	3033
	PLACE60068710	1064	363..1139	3034
25	PLACE60069880	1065	898..1374	3035
	PLACE60070500	1066	765..1718	3036
	PLACE60071800	1067	689..1333	3037
	PLACE60072390	1068	145..522	3038
	PLACE60072420	1069	289..684	3039
30	PLACE60073090	1070	384..1814	3040
	PLACE60074820	1071	38..727	3041
	PLACE60077870	1072	2280..2609	3042
	PLACE60080360	1073	285..938	3043
35	PLACE60081260	1074	1192..1860	3044
	PLACE60082850	1075	665..1132	3045
	PLACE60087680	1076	3..836	3046
	PLACE60088240	1077	94..570	3047
	PLACE60092280	1078	180..869	3048
40	PLACE60092370	1079	371..691	3049
	PLACE60093380	1080	433..1335	3050
	PLACE60095240	1081	956..1312	3051
	PLACE60095600	1082	4..>2605	3052
45	PLACE60098350	1083	86..1852	3053
	PLACE60104630	1084	1267..1671	3054
	PLACE60105680	1085	1290..1631	3055
	PLACE60107010	1086	128..829	3056
	PLACE60109910	1087	4..567	3057
50	PLACE60113340	1088	127..1518	3058
	PLACE60118810	1089	101..1657	3059
	PLACE60119700	1090	199..516	3060
	PLACE60120280	1091	61..705	3061
55	PLACE60122970	1092	861..>1396	3062
	PLACE60132200	1093	240..1082	3063
	PLACE60132320	1094	471..1121	3064
	PLACE60132880	1095	495..1406	3065

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	PLACE60138840	1096	729..1553	3066
	PLACE60140640	1097	840..1919	3067
	PLACE60150510	1098	215..1246	3068
	PLACE60154450	1099	25..873	3069
	PLACE60155910	1100	255..701	3070
10	PLACE60157310	1101	1156..1482	3071
	PLACE60162100	1102	885..1226	3072
	PLACE60175640	1103	242..556	3073
	PLACE60177880	1104	104..1327	3074
15	PLACE60177910	1105	59..442	3075
	PLACE60181870	1106	131..673	3076
	PLACE60184410	1107	995..1483	3077
	PLACE60184870	1108	86..>1402	3078
	PLACE60188630	1109	571..1395	3079
20	PROST10001100	1110	716..1219	3080
	PROST10001360	1111	1506..1997	3081
	PROST10002150	1112	840..2345	3082
	PROST20007170	1113	216..1679	3083
25	PROST20007600	1114	29..742	3084
	PROST20011160	1115	150..548	3085
	PROST20011800	1116	1297..1629	3086
	PROST20014140	1117	1901..3022	3087
	PROST20014150	1118	1632..1961	3088
30	PROST20014650	1119	1243..1653	3089
	PROST20015210	1120	711..1499	3090
	PROST20015400	1121	49..399	3091
	PROST20016760	1122	62..1870	3092
35	PROST20022120	1123	301..762	3093
	PROST20024250	1124	38..445	3094
	PROST20028970	1125	30..821	3095
	PROST20033240	1126	39..1682	3096
	PROST20035170	1127	689..1078	3097
40	PROST20035830	1128	1154..1468	3098
	PROST20036280	1129	1801..2295	3099
	PROST20036350	1130	22..2175	3100
	PROST20039300	1131	87..635	3101
45	PROST20041460	1132	427..855	3102
	PROST20042700	1133	461..1081	3103
	PROST20045700	1134	472..975	3104
	PROST20047440	1135	1058..1441	3105
	PROST20048170	1136	73..555	3106
50	PROST20050390	1137	1358..2035	3107
	PROST20051310	1138	1913..2737	3108
	PROST20052720	1139	1195..1515	3109
	PROST20052850	1140	430..1185	3110
55	PROST20054660	1141	55..753	3111
	PROST20058860	1142	506..892	3112
	PROST20060200	1143	103..429	3113
	PROST20062820	1144	415..1215	3114

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	PROST20063430	1145	126..1199	3115
	PROST20065100	1146	95..1522	3116
	PROST20065790	1147	225..2555	3117
	PROST20073280	1148	891..1277	3118
	PROST20075280	1149	97..885	3119
10	PROST20078710	1150	347..1213	3120
	PROST20082430	1151	2077..2436	3121
	PROST20084470	1152	728..1498	3122
	PROST20084680	1153	395..733	3123
15	PROST20084720	1154	1528..1839	3124
	PROST20087240	1155	766..1452	3125
	PROST20093470	1156	1288..1647	3126
	PROST20094000	1157	376..1011	3127
	PROST20097310	1158	1502..1903	3128
20	PROST20097360	1159	99..602	3129
	PROST20097840	1160	687..1289	3130
	PROST20099090	1161	85..792	3131
	PROST20102190	1162	86..406	3132
25	PROST20102500	1163	1467..2051	3133
	PROST20103820	1164	1770..2078	3134
	PROST20105450	1165	1027..1911	3135
	PROST20106060	1166	97..705	3136
	PROST20108850	1167	1173..1664	3137
30	PROST20110120	1168	804..1139	3138
	PROST20114100	1169	74..772	3139
	PROST20120070	1170	442..1593	3140
	PROST20121570	1171	673..1185	3141
35	PROST20122490	1172	10..753	3142
	PROST20124000	1173	943..1371	3143
	PROST20125420	1174	1480..1968	3144
	PROST20127450	1175	255..857	3145
	PROST20130320	1176	549..2309	3146
40	PROST20138730	1177	494..829	3147
	PROST20146590	1178	618..2351	3148
	PROST20151370	1179	99..482	3149
	PROST20152510	1180	1095..2168	3150
45	PROST20152870	1181	258..1322	3151
	PROST20155370	1182	606..2255	3152
	PROST20156360	1183	1557..1898	3153
	PROST20159320	1184	67..567	3154
	PROST20168600	1185	336..1700	3155
50	PUAEN10000650	1186	341..943	3156
	PUAEN10000870	1187	1676..2029	3157
	PUAEN10001640	1188	332..1138	3158
	PUAEN20000800	1189	327..1811	3159
55	PUAEN20001520	1190	155..1243	3160
	PUAEN20002470	1191	3..2417	3161
	PUAEN20003120	1192	93..2216	3162
	SALGL10001070	1193	89..997	3163

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SKMUS20006790	1194	389..1330	3164
	SKMUS20007260	1195	47..>1320	3165
	SKMUS20008730	1196	91..1407	3166
	SKMUS20017400	1197	84..815	3167
	SKMUS20020770	1198	179..781	3168
10	SKMUS20026340	1199	57..1202	3169
	SKMUS20040440	1200	27..1091	3170
	SKMUS20064810	1201	91..459	3171
	SKMUS20073150	1202	17..>822	3172
15	SKMUS20073590	1203	438..824	3173
	SKMUS20079150	1204	165..1235	3174
	SKMUS20091900	1205	57..359	3175
	SKNMC10001230	1206	87..1814	3176
	SKNMC20006350	1207	326..1738	3177
20	SKNSH10001010	1208	1189..1530	3178
	SKNSH20007160	1209	113..562	3179
	SKNSH20009710	1210	71..622	3180
	SKNSH20030640	1211	1635..2090	3181
25	SKNSH20040390	1212	246..911	3182
	SKNSH20052400	1213	926..2017	3183
	SKNSH20057920	1214	369..1352	3184
	SKNSH20068220	1215	504..1235	3185
	SKNSH20094350	1216	70..591	3186
30	SMINT20000070	1217	752..1858	3187
	SMINT20002320	1218	607..1761	3188
	SMINT20006020	1219	1215..2348	3189
	SMINT20006090	1220	75..602	3190
35	SMINT20007470	1221	154..1650	3191
	SMINT20008110	1222	784..1557	3192
	SMINT20011830	1223	34..447	3193
	SMINT20011950	1224	732..2006	3194
	SMINT20012220	1225	239..616	3195
40	SMINT20013970	1226	1117..1686	3196
	SMINT20014610	1227	287..814	3197
	SMINT20016150	1228	911..1675	3198
	SMINT20017310	1229	1220..1561	3199
45	SMINT20021260	1230	1066..1407	3200
	SMINT20023110	1231	1696..2073	3201
	SMINT20024140	1232	31..555	3202
	SMINT20026200	1233	323..2170	3203
	SMINT20028800	1234	476..1696	3204
50	SMINT20028840	1235	89..823	3205
	SMINT20030740	1236	172..1833	3206
	SMINT20031280	1237	542..1489	3207
	SMINT20035050	1238	227..2149	3208
55	SMINT20035510	1239	168..>1891	3209
	SMINT20036440	1240	207..2084	3210
	SMINT20038660	1241	289..1449	3211
	SMINT20039050	1242	175..>2338	3212

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SMINT20043390	1243	1465..2094	3213
	SMINT20044140	1244	30..1718	3214
	SMINT20044730	1245	45..1787	3215
	SMINT20045470	1246	1156..1539	3216
	SMINT20045830	1247	287..1882	3217
10	SMINT20045890	1248	893..1372	3218
	SMINT20047290	1249	2..637	3219
	SMINT20048720	1250	1834..>2374	3220
	SMINT20049920	1251	1384..1860	3221
15	SMINT20052130	1252	271..891	3222
	SMINT20054050	1253	361..1839	3223
	SMINT20056230	1254	73..1674	3224
	SMINT20056240	1255	1108..1533	3225
	SMINT20062050	1256	75..1964	3226
20	SMINT20067080	1257	138..2075	3227
	SMINT20070620	1258	44..445	3228
	SMINT20074330	1259	71..532	3229
	SMINT20077920	1260	843..1166	3230
25	SMINT20077960	1261	1010..2467	3231
	SMINT20081330	1262	250..618	3232
	SMINT20083290	1263	80..1606	3233
	SMINT20084910	1264	664..987	3234
	SMINT20085310	1265	129..500	3235
30	SMINT20085450	1266	66..437	3236
	SMINT20086250	1267	1958..2287	3237
	SMINT20086720	1268	233..1003	3238
	SMINT20088440	1269	31..438	3239
35	SMINT20088690	1270	26..580	3240
	SMINT20089210	1271	1259..1672	3241
	SMINT20089600	1272	241..1335	3242
	SMINT20091190	1273	290..1765	3243
	SMINT20092120	1274	33..416	3244
40	SMINT20092160	1275	439..780	3245
	SMINT20093630	1276	1822..2241	3246
	SMINT20094150	1277	511..966	3247
	SMINT20094680	1278	36..452	3248
45	SPLEN20005160	1279	2342..2659	3249
	SPLEN20005370	1280	1497..1856	3250
	SPLEN20006950	1281	702..1343	3251
	SPLEN20011350	1282	1127..1537	3252
	SPLEN20012450	1283	134..442	3253
50	SPLEN20015030	1284	376..945	3254
	SPLEN20015100	1285	1367..2137	3255
	SPLEN20016500	1286	328..816	3256
	SPLEN20017610	1287	940..1314	3257
55	SPLEN20017810	1288	101..556	3258
	SPLEN20019120	1289	176..487	3259
	SPLEN20020530	1290	358..762	3260
	SPLEN20023430	1291	1067..1426	3261

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SPLEN20023540	1292	644..1903	3262
	SPLEN20023850	1293	467..>1879	3263
	SPLEN20024190	1294	319..1368	3264
	SPLEN20024510	1295	1070..1423	3265
	SPLEN20024620	1296	3..1514	3266
10	SPLEN20024770	1297	134..2353	3267
	SPLEN20024930	1298	1150..3069	3268
	SPLEN20029170	1299	67..750	3269
	SPLEN20036780	1300	1432..1752	3270
15	SPLEN20039180	1301	359..1534	3271
	SPLEN20040780	1302	1675..2346	3272
	SPLEN20041810	1303	801..1142	3273
	SPLEN20042200	1304	1123..1935	3274
	SPLEN20043430	1305	224..565	3275
20	SPLEN20043460	1306	55..1899	3276
	SPLEN20043680	1307	1337..2371	3277
	SPLEN20045550	1308	5..1513	3278
	SPLEN20048800	1309	2038..2352	3279
25	SPLEN20049840	1310	82..3378	3280
	SPLEN20050090	1311	418..2202	3281
	SPLEN20051420	1312	685..1983	3282
	SPLEN20054160	1313	186..2069	3283
	SPLEN20054500	1314	667..1443	3284
30	SPLEN20055600	1315	146..1033	3285
	SPLEN20057830	1316	507..1163	3286
	SPLEN20057900	1317	1883..2431	3287
	SPLEN20058180	1318	803..1120	3288
35	SPLEN20059270	1319	162..1586	3289
	SPLEN20062830	1320	282..785	3290
	SPLEN20063250	1321	315..1535	3291
	SPLEN20063890	1322	133..996	3292
	SPLEN20067010	1323	2702..>3023	3293
40	SPLEN20071820	1324	876..1592	3294
	SPLEN20073500	1325	174..2210	3295
	SPLEN20073880	1326	220..2595	3296
	SPLEN20076190	1327	20..331	3297
45	SPLEN20076470	1328	575..1714	3298
	SPLEN20080070	1329	5..1339	3299
	SPLEN20081640	1330	946..1308	3300
	SPLEN20085910	1331	1084..1434	3301
	SPLEN20087370	1332	2670..3098	3302
50	SPLEN20087860	1333	255..755	3303
	SPLEN20090880	1334	1742..2194	3304
	SPLEN20098030	1335	268..1077	3305
	SPLEN20100040	1336	101..862	3306
55	SPLEN20101950	1337	122..1198	3307
	SPLEN20104150	1338	1146..2219	3308
	SPLEN20104690	1339	661..990	3309
	SPLEN20105100	1340	1425..1859	3310

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SPLEN20108000	1341	887..1351	3311
	SPLEN20108460	1342	2254..2607	3312
	SPLEN20110180	1343	147..1292	3313
	SPLEN20110210	1344	1831..2271	3314
	SPLEN20110860	1345	1489..1887	3315
10	SPLEN20111450	1346	2768..3208	3316
	SPLEN20114190	1347	154..1440	3317
	SPLEN20116720	1348	9..1583	3318
	SPLEN20117580	1349	218..1240	3319
15	SPLEN20118050	1350	145..1122	3320
	SPLEN20121790	1351	569..1054	3321
	SPLEN20125230	1352	971..1324	3322
	SPLEN20126110	1353	254..991	3323
	SPLEN20135030	1354	40..1848	3324
20	SPLEN20136700	1355	1296..1628	3325
	SPLEN20136730	1356	1312..1644	3326
	SPLEN20137530	1357	2676..3221	3327
	SPLEN20138600	1358	1166..1582	3328
25	SPLEN20139100	1359	63..1532	3329
	SPLEN20139360	1360	763..1827	3330
	SPLEN20175920	1361	1123..1590	3331
	SPLEN20176130	1362	16..549	3332
	SPLEN20177400	1363	1078..1431	3333
30	SPLEN20180980	1364	410..823	3334
	SPLEN20181570	1365	214..>2609	3335
	SPLEN20182850	1366	168..659	3336
	SPLEN20182990	1367	55..1881	3337
35	SPLEN20183020	1368	265..723	3338
	SPLEN20183950	1369	402..746	3339
	SPLEN20187490	1370	98..>2458	3340
	SPLEN20190080	1371	914..1342	3341
	SPLEN20190430	1372	884..>1942	3342
40	SPLEN20190770	1373	97..771	3343
	SPLEN20191020	1374	140..1426	3344
	SPLEN20192570	1375	325..654	3345
	SPLEN20193230	1376	253..588	3346
45	SPLEN20193490	1377	321..854	3347
	SPLEN20193750	1378	845..1306	3348
	SPLEN20193790	1379	290..2278	3349
	SPLEN20195710	1380	64..516	3350
	SPLEN20197090	1381	11..550	3351
50	SPLEN20197740	1382	2..499	3352
	SPLEN20197930	1383	803..>1625	3353
	SPLEN20198390	1384	14..1873	3354
	SPLEN20199850	1385	575..1009	3355
55	SPLEN20200070	1386	353..655	3356
	SPLEN20200340	1387	1047..1814	3357
	SPLEN20201830	1388	143..1177	3358
	SPLEN20203590	1389	160..471	3359

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SPLN20204670	1390	6..311	3360
	SPLN20205120	1391	682..1542	3361
	TESOP10000350	1392	1646..2101	3362
	TESOP10001600	1393	282..1352	3363
	TESTI10000190	1394	84..2042	3364
10	TESTI10000850	1395	925..1311	3365
	TESTI10001570	1396	141..1919	3366
	TESTI20004310	1397	55..2484	3367
	TESTI20005980	1398	1350..>1866	3368
15	TESTI20006160	1399	53..1720	3369
	TESTI20006830	1400	313..1719	3370
	TESTI20012080	1401	89..1867	3371
	TESTI20012360	1402	178..594	3372
	TESTI20016970	1403	133..1842	3373
20	TESTI20019590	1404	210..752	3374
	TESTI20028020	1405	201..1298	3375
	TESTI20029100	1406	1743..2147	3376
	TESTI20030200	1407	94..2091	3377
25	TESTI20030440	1408	60..1931	3378
	TESTI20030610	1409	547..1371	3379
	TESTI20031310	1410	889..2235	3380
	TESTI20031410	1411	201..1655	3381
	TESTI20032770	1412	163..1002	3382
30	TESTI20034750	1413	472..804	3383
	TESTI20035330	1414	13..558	3384
	TESTI20035790	1415	16..2163	3385
	TESTI20038240	1416	163..2502	3386
35	TESTI20040850	1417	52..669	3387
	TESTI20041630	1418	330..1526	3388
	TESTI20043130	1419	410..715	3389
	TESTI20043180	1420	68..2515	3390
	TESTI20043220	1421	1496..1957	3391
40	TESTI20043910	1422	37..1728	3392
	TESTI20043990	1423	311..1153	3393
	TESTI20044900	1424	234..1595	3394
	TESTI20045390	1425	156..2108	3395
45	TESTI20045740	1426	199..549	3396
	TESTI20046110	1427	24..1826	3397
	TESTI20046490	1428	554..2542	3398
	TESTI20046540	1429	123..2309	3399
	TESTI20046870	1430	278..1645	3400
50	TESTI20046890	1431	276..2702	3401
	TESTI20047370	1432	2..2134	3402
	TESTI20047930	1433	239..1843	3403
	TESTI20049060	1434	1191..1784	3404
55	TESTI20049410	1435	281..2170	3405
	TESTI20049990	1436	355..915	3406
	TESTI20050170	1437	314..808	3407
	TESTI20050400	1438	111..440	3408

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20050720	1439	68..1621	3409
	TESTI20051200	1440	1561..2145	3410
	TESTI20051730	1441	183..1943	3411
	TESTI20052670	1442	759..1910	3412
10	TESTI20053070	1443	98..1285	3413
	TESTI20053260	1444	456..842	3414
	TESTI20053780	1445	176..1948	3415
	TESTI20053800	1446	42..1694	3416
	TESTI20053950	1447	528..>1782	3417
15	TESTI20054700	1448	19..1956	3418
	TESTI20055680	1449	53..1510	3419
	TESTI20055880	1450	127..1644	3420
	TESTI20056030	1451	543..1658	3421
	TESTI20057200	1452	279..611	3422
20	TESTI20057430	1453	131..1858	3423
	TESTI20057590	1454	37..1062	3424
	TESTI20057840	1455	180..1271	3425
	TESTI20057880	1456	39..1697	3426
25	TESTI20058350	1457	25..1368	3427
	TESTI20058920	1458	108..1088	3428
	TESTI20059080	1459	2134..3069	3429
	TESTI20059330	1460	540..845	3430
	TESTI20059370	1461	655..1137	3431
30	TESTI20059480	1462	52..1362	3432
	TESTI20059790	1463	203..1336	3433
	TESTI20059810	1464	324..>1914	3434
	TESTI20060080	1465	172..858	3435
35	TESTI20060150	1466	383..1663	3436
	TESTI20060350	1467	81..1427	3437
	TESTI20060450	1468	1306..1752	3438
	TESTI20060830	1469	54..2543	3439
	TESTI20061090	1470	382..798	3440
40	TESTI20061200	1471	382..1938	3441
	TESTI20062120	1472	37..1632	3442
	TESTI20062180	1473	169..1413	3443
	TESTI20062580	1474	863..1165	3444
45	TESTI20063330	1475	1334..1678	3445
	TESTI20063410	1476	2175..2501	3446
	TESTI20063600	1477	1399..1809	3447
	TESTI20064370	1478	201..1706	3448
	TESTI20064530	1479	68..2737	3449
50	TESTI20064650	1480	353..2542	3450
	TESTI20064990	1481	733..1290	3451
	TESTI20065650	1482	374..1609	3452
	TESTI20066150	1483	98..2473	3453
55	TESTI20066170	1484	143..1309	3454
	TESTI20066280	1485	100..879	3455
	TESTI20066330	1486	26..1528	3456
	TESTI20066590	1487	306..740	3457

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20066650	1488	415..1362	3458
	TESTI20067350	1489	342..1073	3459
	TESTI20067440	1490	196..1887	3460
	TESTI20067480	1491	127..1758	3461
	TESTI20068530	1492	791..1369	3462
10	TESTI20068790	1493	1033..>1738	3463
	TESTI20068940	1494	55..>1867	3464
	TESTI20070400	1495	147..2300	3465
	TESTI20070740	1496	743..1480	3466
15	TESTI20071130	1497	224..1738	3467
	TESTI20071630	1498	38..727	3468
	TESTI20073460	1499	97..1584	3469
	TESTI20075240	1500	259..1686	3470
	TESTI20076570	1501	622..1110	3471
20	TESTI20076920	1502	90..608	3472
	TESTI20079060	1503	105..2096	3473
	TESTI20079220	1504	54..2252	3474
	TESTI20079980	1505	62..1300	3475
25	TESTI20080460	1506	1458..1787	3476
	TESTI20081890	1507	184..2520	3477
	TESTI20083890	1508	1102..1596	3478
	TESTI20084250	1509	386..2035	3479
	TESTI20085670	1510	1459..2001	3480
30	TESTI20086840	1511	10..1488	3481
	TESTI20088840	1512	172..1587	3482
	TESTI20089290	1513	26..421	3483
	TESTI20090180	1514	527..1657	3484
35	TESTI20090970	1515	548..2308	3485
	TESTI20091360	1516	745..1230	3486
	TESTI20092170	1517	882..1256	3487
	TESTI20093900	1518	265..1791	3488
	TESTI20094620	1519	1897..2319	3489
40	TESTI20095200	1520	94..1149	3490
	TESTI20095440	1521	1134..1496	3491
	TESTI20095770	1522	278..>2225	3492
	TESTI20095880	1523	144..1775	3493
45	TESTI20097270	1524	157..693	3494
	TESTI20099350	1525	123..>1773	3495
	TESTI20100090	1526	1020..2057	3496
	TESTI20102390	1527	1873..2247	3497
	TESTI20103690	1528	71..1048	3498
50	TESTI20104090	1529	364..1716	3499
	TESTI20105130	1530	320..1966	3500
	TESTI20105910	1531	151..2265	3501
	TESTI20106170	1532	235..1338	3502
55	TESTI20106820	1533	1191..1604	3503
	TESTI20107240	1534	163..2844	3504
	TESTI20107320	1535	377..787	3505
	TESTI20107340	1536	1229..1723	3506

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20108060	1537	371..925	3507
	TESTI20112540	1538	148..1554	3508
	TESTI20112860	1539	285..1829	3509
	TESTI20113150	1540	374..1042	3510
	TESTI20113940	1541	1185..1598	3511
10	TESTI20114480	1542	161..2032	3512
	TESTI20116050	1543	218..1756	3513
	TESTI20116120	1544	17..1276	3514
	TESTI20117500	1545	140..508	3515
15	TESTI20118460	1546	69..1580	3516
	TESTI20120500	1547	135..926	3517
	TESTI20120900	1548	60..665	3518
	TESTI20121040	1549	8..1525	3519
	TESTI20121710	1550	278..1543	3520
20	TESTI20122070	1551	145..1359	3521
	TESTI20122440	1552	25..465	3522
	TESTI20124440	1553	469..801	3523
	TESTI20125280	1554	371..1363	3524
25	TESTI20125440	1555	342..671	3525
	TESTI20125920	1556	31..1680	3526
	TESTI20126280	1557	169..2562	3527
	TESTI20130530	1558	298..1692	3528
	TESTI20131440	1559	223..1278	3529
30	TESTI20132310	1560	204..713	3530
	TESTI20132680	1561	1011..1448	3531
	TESTI20134010	1562	334..1464	3532
	TESTI20134270	1563	59..601	3533
35	TESTI20134680	1564	324..2726	3534
	TESTI20134970	1565	197..1873	3535
	TESTI20136010	1566	152..1415	3536
	TESTI20140970	1567	376..801	3537
	TESTI20142480	1568	1466..1939	3538
40	TESTI20142540	1569	1231..1593	3539
	TESTI20143180	1570	201..1946	3540
	TESTI20144390	1571	776..1552	3541
	TESTI20145780	1572	1315..1746	3542
45	TESTI20148380	1573	32..2680	3543
	TESTI20149880	1574	581..982	3544
	TESTI20150420	1575	221..1162	3545
	TESTI20150920	1576	142..1713	3546
	TESTI20151050	1577	1290..1736	3547
50	TESTI20151800	1578	671..1099	3548
	TESTI20152490	1579	717..1226	3549
	TESTI20153310	1580	151..1317	3550
	TESTI20154370	1581	192..1544	3551
55	TESTI20159380	1582	852..1679	3552
	TESTI20161010	1583	33..539	3553
	TESTI20162780	1584	607..1299	3554
	TESTI20162980	1585	224..1414	3555

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20164210	1586	526..1593	3556
	TESTI20165680	1587	154..552	3557
	TESTI20165990	1588	201..992	3558
	TESTI20166290	1589	351..2786	3559
	TESTI20166670	1590	754..1938	3560
10	TESTI20167580	1591	1152..>1543	3561
	TESTI20168880	1592	201..524	3562
	TESTI20169500	1593	280..1674	3563
	TESTI20170170	1594	199..1530	3564
15	TESTI20170280	1595	1..696	3565
	TESTI20170690	1596	61..474	3566
	TESTI20170890	1597	882..1238	3567
	TESTI20171070	1598	1088..1501	3568
	TESTI20173050	1599	724..1218	3569
20	TESTI20173110	1600	1194..1586	3570
	TESTI20173960	1601	376..1764	3571
	TESTI20175370	1602	828..1724	3572
	TESTI20176450	1603	1..996	3573
25	TESTI20179230	1604	162..1709	3574
	TESTI20179510	1605	1702..>2042	3575
	TESTI20180600	1606	162..857	3576
	TESTI20182210	1607	736..1182	3577
	TESTI20182760	1608	266..1390	3578
30	TESTI20183680	1609	778..>1927	3579
	TESTI20184280	1610	35..>1732	3580
	TESTI20184750	1611	899..2116	3581
	TESTI20184760	1612	161..1741	3582
35	TESTI20184820	1613	189..722	3583
	TESTI20186110	1614	221..1606	3584
	TESTI20192570	1615	109..687	3585
	TESTI20193080	1616	149..2194	3586
	TESTI20193520	1617	311..1375	3587
40	TESTI20194880	1618	616..1554	3588
	TESTI20196690	1619	271..945	3589
	TESTI20196970	1620	789..1565	3590
	TESTI20197030	1621	263..1717	3591
45	TESTI20197290	1622	643..1314	3592
	TESTI20197600	1623	100..909	3593
	TESTI20198540	1624	21..1553	3594
	TESTI20198600	1625	909..1328	3595
	TESTI20199110	1626	622..1617	3596
50	TESTI20199980	1627	764..1102	3597
	TESTI20200120	1628	661..966	3598
	TESTI20200840	1629	378..818	3599
	TESTI20201760	1630	22..603	3600
55	TESTI20202830	1631	631..972	3601
	TESTI20204260	1632	714..1406	3602
	TESTI20205100	1633	270..1763	3603
	TESTI20205150	1634	1286..1663	3604

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20205250	1635	32..1888	3605
	TESTI20207170	1636	1..795	3606
	TESTI20209050	1637	269..1900	3607
	TESTI20210030	1638	328..675	3608
	TESTI20210570	1639	280..1362	3609
10	TESTI20211380	1640	372..848	3610
	TESTI20212970	1641	93..2102	3611
	TESTI20214630	1642	690..1106	3612
	TESTI20215310	1643	294..899	3613
15	TESTI20219110	1644	982..1344	3614
	TESTI20219390	1645	253..573	3615
	TESTI20220230	1646	116..967	3616
	TESTI20221790	1647	109..1830	3617
	TESTI20222030	1648	277..2277	3618
20	TESTI20222460	1649	162..1889	3619
	TESTI20223380	1650	322..831	3620
	TESTI20226520	1651	178..1392	3621
	TESTI20227380	1652	20..1747	3622
25	TESTI20228120	1653	31..858	3623
	TESTI20228740	1654	607..1026	3624
	TESTI20244220	1655	757..2448	3625
	TESTI20244430	1656	17..1444	3626
	TESTI20244460	1657	684..1511	3627
30	TESTI20244730	1658	127..1044	3628
	TESTI20245600	1659	255..1523	3629
	TESTI20245860	1660	684..1058	3630
	TESTI20246410	1661	1513..1818	3631
35	TESTI20246480	1662	380..1399	3632
	TESTI20247440	1663	425..907	3633
	TESTI20248850	1664	3..1829	3634
	TESTI20249360	1665	600..1565	3635
	TESTI20250220	1666	63..2015	3636
40	TESTI20250630	1667	482..1690	3637
	TESTI20251440	1668	42..1271	3638
	TESTI20251610	1669	430..1218	3639
	TESTI20251740	1670	730..1104	3640
45	TESTI20252690	1671	1182..2138	3641
	TESTI20254030	1672	363..1958	3642
	TESTI20254090	1673	878..1360	3643
	TESTI20254480	1674	320..1390	3644
	TESTI20254990	1675	693..1799	3645
50	TESTI20255460	1676	152..2710	3646
	TESTI20256560	1677	169..>2257	3647
	TESTI20257910	1678	457..1311	3648
	TESTI20258720	1679	38..1630	3649
55	TESTI20259110	1680	486..1805	3650
	TESTI20259200	1681	227..1369	3651
	TESTI20260140	1682	1113..1421	3652
	TESTI20260640	1683	6..1109	3653

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20261040	1684	14..970	3654
	TESTI20261160	1685	257..868	3655
	TESTI20261680	1686	1422..1901	3656
	TESTI20262150	1687	315..2765	3657
	TESTI20262940	1688	255..1574	3658
10	TESTI20264530	1689	150..1580	3659
	TESTI20264910	1690	1638..2378	3660
	TESTI20265150	1691	1023..1409	3661
	TESTI20265340	1692	965..1552	3662
15	TESTI20265890	1693	994..1308	3663
	TESTI20266050	1694	116..1522	3664
	TESTI20268240	1695	70..1638	3665
	TESTI20269250	1696	17..>1926	3666
	TESTI20269360	1697	682..1005	3667
20	TESTI20270130	1698	99..512	3668
	TESTI20271790	1699	101..1822	3669
	TESTI20272380	1700	121..492	3670
	TESTI20274960	1701	619..1716	3671
25	TESTI20277300	1702	263..1600	3672
	TESTI20278280	1703	80..607	3673
	TESTI20282420	1704	52..528	3674
	TESTI20282530	1705	699..1985	3675
	TESTI20282900	1706	30..341	3676
30	TESTI20284260	1707	29..493	3677
	TESTI20285230	1708	1710..2366	3678
	TESTI20286590	1709	519..1121	3679
	TESTI20287760	1710	775..2634	3680
35	THYMU10004280	1711	617..988	3681
	THYMU20006020	1712	608..1387	3682
	THYMU20007020	1713	1755..2111	3683
	THYMU20007750	1714	1077..1499	3684
	THYMU20008000	1715	1506..1955	3685
40	THYMU20009460	1716	1334..1723	3686
	THYMU20009500	1717	717..2117	3687
	THYMU20009710	1718	247..762	3688
	THYMU20010180	1719	191..634	3689
45	THYMU20010710	1720	850..1164	3690
	THYMU20012020	1721	1160..1561	3691
	THYMU20012560	1722	47..517	3692
	THYMU20013250	1723	131..1309	3693
	THYMU20013810	1724	196..927	3694
50	THYMU20014430	1725	1280..1678	3695
	THYMU20017270	1726	16..660	3696
	THYMU20018250	1727	1205..2122	3697
	THYMU20018390	1728	237..1373	3698
	THYMU20019000	1729	405..758	3699
55	THYMU20019260	1730	317..736	3700
	THYMU20020370	1731	1332..1733	3701
	THYMU20020800	1732	600..1196	3702

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	THYMU20021090	1733	211..1281	3703
	THYMU20021540	1734	100..1578	3704
	THYMU20023560	1735	1429..1884	3705
	THYMU20024500	1736	199..1584	3706
	THYMU20025480	1737	1362..1751	3707
10	THYMU20026950	1738	9..920	3708
	THYMU20028150	1739	233..1222	3709
	THYMU20028410	1740	10..1086	3710
	THYMU20029830	1741	46..456	3711
15	THYMU20030460	1742	453..1175	3712
	THYMU20030690	1743	1658..2269	3713
	THYMU20031330	1744	90..569	3714
	THYMU20032820	1745	250..1176	3715
	THYMU20034400	1746	791..1123	3716
20	THYMU20034790	1747	120..452	3717
	THYMU20036500	1748	56..1657	3718
	THYMU20039320	1749	584..1339	3719
	THYMU20043440	1750	1301..1615	3720
25	THYMU20043560	1751	292..621	3721
	THYMU20044100	1752	1800..2228	3722
	THYMU20044520	1753	1387..1899	3723
	THYMU20046350	1754	1863..2351	3724
	THYMU20046770	1755	321..671	3725
30	THYMU20049060	1756	172..732	3726
	THYMU20050010	1757	206..1681	3727
	THYMU20051340	1758	886..1209	3728
	THYMU20052460	1759	1300..1683	3729
35	THYMU20052830	1760	92..1504	3730
	THYMU20054800	1761	479..880	3731
	THYMU20055450	1762	112..426	3732
	THYMU20055460	1763	20..361	3733
	THYMU20055740	1764	901..1341	3734
40	THYMU20055760	1765	232..738	3735
	THYMU20058550	1766	1170..1493	3736
	THYMU20060480	1767	2046..>2453	3737
	THYMU20062520	1768	299..655	3738
45	THYMU20062610	1769	136..1953	3739
	THYMU20062770	1770	381..1199	3740
	THYMU20063650	1771	264..800	3741
	THYMU20064680	1772	253..621	3742
	THYMU20066660	1773	405..1487	3743
50	THYMU20069130	1774	341..961	3744
	THYMU20069460	1775	231..575	3745
	THYMU20069650	1776	728..1036	3746
	THYMU20070250	1777	81..1703	3747
55	THYMU20071120	1778	170..1792	3748
	THYMU20071460	1779	152..499	3749
	THYMU20072580	1780	1981..2286	3750
	THYMU20073070	1781	551..1225	3751

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	THYMU20073080	1782	755..1198	3752
	THYMU20077250	1783	645..1241	3753
	THYMU20078020	1784	1290..1598	3754
	THYMU20078240	1785	1506..1838	3755
	THYMU20079690	1786	1049..1714	3756
10	THYMU20080490	1787	57..398	3757
	THYMU20081110	1788	629..1246	3758
	THYMU20083390	1789	592..924	3759
	THYMU20083500	1790	744..1067	3760
15	THYMU20083830	1791	155..1786	3761
	THYMU20084520	1792	286..597	3762
	THYMU20086430	1793	769..1077	3763
	THYMU20087270	1794	842..2008	3764
	THYMU20089170	1795	305..619	3765
20	THYMU20089900	1796	1008..1421	3766
	THYMU20090230	1797	106..594	3767
	THYMU20091040	1798	728..1054	3768
	THYMU20095920	1799	1809..2378	3769
25	THYMU20096580	1800	120..692	3770
	THYMU20097920	1801	95..2086	3771
	THYMU20098350	1802	99..1802	3772
	THYMU20099060	1803	80..1573	3773
30	THYMU20100940	1804	8..2218	3774
	THYMU20104480	1805	39..1451	3775
	THYMU20106990	1806	673..1464	3776
	THYMU20110720	1807	372..1070	3777
	THYMU20112570	1808	117..455	3778
35	THYMU20112590	1809	112..1827	3779
	THYMU20115380	1810	1507..1839	3780
	THYMU20115730	1811	943..1632	3781
	THYMU20117850	1812	1625..1948	3782
	THYMU20120240	1813	1239..3002	3783
40	THYMU20120730	1814	1257..2459	3784
	THYMU20121040	1815	230..2323	3785
	THYMU20128910	1816	181..1185	3786
	THYMU20129020	1817	1545..>2019	3787
45	THYMU20130470	1818	87..1169	3788
	THYMU20134260	1819	1845..2171	3789
	THYMU20137050	1820	958..1341	3790
	THYMU20137570	1821	2113..2571	3791
	THYMU20139160	1822	69..686	3792
50	THYMU20140510	1823	1312..1626	3793
	THYMU20143230	1824	575..2023	3794
	THYMU20145990	1825	1330..2262	3795
	THYMU20148010	1826	326..820	3796
55	THYMU20149230	1827	581..925	3797
	THYMU20150190	1828	1516..1908	3798
	THYMU20151610	1829	218..1663	3799
	THYMU20153210	1830	1135..2340	3800

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	THYMU20154790	1831	1220..1753	3801
	THYMU20157620	1832	771..1487	3802
	THYMU20163600	1833	1216..1650	3803
	THYMU20170080	1834	944..1399	3804
	THYMU20170230	1835	835..1941	3805
10	THYMU20171580	1836	821..1150	3806
	THYMU20174490	1837	52..453	3807
	THYMU20174790	1838	29..370	3808
	THYMU20175260	1839	991..1452	3809
15	THYMU20176010	1840	12..2039	3810
	THYMU20177070	1841	1059..1415	3811
	THYMU20178440	1842	81..1517	3812
	THYMU20181890	1843	102..1652	3813
	THYMU20184550	1844	171..1886	3814
20	THYMU20185470	1845	161..817	3815
	THYMU20185650	1846	36..536	3816
	THYMU20187210	1847	190..507	3817
	THYMU20191970	1848	230..1597	3818
25	TKIDN10000620	1849	1075..1419	3819
	TKIDN10001710	1850	1685..2365	3820
	TKIDN10001920	1851	98..793	3821
	TRACH20011010	1852	228..2033	3822
	TRACH20011540	1853	125..478	3823
30	TRACH20012490	1854	83..1600	3824
	TRACH20021000	1855	234..854	3825
	TRACH20021380	1856	313..1890	3826
	TRACH20025370	1857	947..1456	3827
35	TRACH20026640	1858	964..1557	3828
	TRACH20029880	1859	201..1607	3829
	TRACH20040390	1860	125..3319	3830
	TRACH20041090	1861	1254..1589	3831
	TRACH20043360	1862	30..2066	3832
40	TRACH20044990	1863	209..790	3833
	TRACH20049500	1864	840..1166	3834
	TRACH20051590	1865	927..1247	3835
	TRACH20057200	1866	2082..2393	3836
45	TRACH20058000	1867	187..1647	3837
	TRACH20073990	1868	98..454	3838
	TRACH20080810	1869	2073..>2910	3839
	TRACH20081270	1870	1681..>2025	3840
	TRACH20090060	1871	309..1781	3841
50	TRACH20091070	1872	129..1841	3842
	TRACH20093400	1873	131..2251	3843
	TRACH20093480	1874	694..1092	3844
	TRACH20098510	1875	142..1944	3845
55	TRACH20101590	1876	1660..2220	3846
	TRACH20104510	1877	144..1184	3847
	TRACH20108240	1878	36..791	3848
	TRACH20113020	1879	177..1352	3849

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TRACH20122980	1880	732..1562	3850
	TRACH20123870	1881	235..540	3851
	TRACH20124970	1882	109..486	3852
	TRACH20125620	1883	22..387	3853
	TRACH20129180	1884	1545..1898	3854
10	TRACH20131230	1885	123..2939	3855
	TRACH20139280	1886	152..1474	3856
	TRACH20140180	1887	203..553	3857
	TRACH20143710	1888	1219..1998	3858
15	TRACH20149500	1889	163..906	3859
	TRACH20149720	1890	187..1695	3860
	TRACH20149740	1891	864..1505	3861
	TRACH20158240	1892	254..796	3862
	TRACH20159390	1893	1618..1941	3863
20	TRACH2016	1894	1223..1531	3864
	TRACH20163470	1895	971..2356	3865
	TRACH20164100	1896	372..722	3866
	TRACH20164810	1897	1685..2104	3867
25	TRACH20165330	1898	704..1102	3868
	TRACH20165540	1899	810..1514	3869
	TRACH20167090	1900	57..1148	3870
	TRACH20170860	1901	186..1625	3871
	TRACH20173680	1902	83..1597	3872
30	TRACH20174980	1903	93..1088	3873
	TRACH20182780	1904	1669..2070	3874
	TRACH2018512	1905	13..339	3875
	TRACH20188350	1906	248..1015	3876
35	TRACH20190460	1907	351..1526	3877
	UMVEN10001380	1908	2122..2436	3878
	UTERU10001060	1909	187..552	3879
	UTERU10001870	1910	1681..2031	3880
	UTERU20000230	1911	120..608	3881
40	UTERU20000950	1912	240..1658	3882
	UTERU20011760	1913	1719..2090	3883
	UTERU20013890	1914	1544..1951	3884
	UTERU20016580	1915	25..1287	3885
45	UTERU20026620	1916	1020..1556	3886
	UTERU20027360	1917	1624..1992	3887
	UTERU20029930	1918	82..1902	3888
	UTERU20031350	1919	35..520	3889
	UTERU20035770	1920	920..1282	3890
50	UTERU20040150	1921	917..1717	3891
	UTERU20040370	1922	22..1866	3892
	UTERU20040390	1923	727..1200	3893
	UTERU20040730	1924	1009..>2303	3894
55	UTERU20041630	1925	105..1328	3895
	UTERU20041970	1926	26..484	3896
	UTERU20045200	1927	6..917	3897
	UTERU20051790	1928	415..1341	3898

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	UTERU20064120	1929	147..1061	3899
	UTERU20065470	1930	389..694	3900
	UTERU20079240	1931	408..713	3901
	UTERU20083020	1932	23..826	3902
	UTERU20086530	1933	1274..1783	3903
10	UTERU20087070	1934	1274..2467	3904
	UTERU20087850	1935	464..991	3905
	UTERU20089300	1936	906..1253	3906
	UTERU20089390	1937	11..1729	3907
15	UTERU20089620	1938	132..725	3908
	UTERU20090940	1939	122..631	3909
	UTERU20091470	1940	260..697	3910
	UTERU20094830	1941	127..1578	3911
	UTERU20095100	1942	1593..1913	3912
20	UTERU20099040	1943	59..883	3913
	UTERU20099510	1944	705..2375	3914
	UTERU20101150	1945	874..1188	3915
	UTERU20102260	1946	270..671	3916
25	UTERU20103040	1947	1164..1772	3917
	UTERU20103200	1948	374..709	3918
	UTERU20104310	1949	90..425	3919
	UTERU20106510	1950	1649..2275	3920
	UTERU20121140	1951	880..1644	3921
30	UTERU20122520	1952	572..>2146	3922
	UTERU20125810	1953	21..329	3923
	UTERU20127030	1954	618..1763	3924
	UTERU20127150	1955	707..1699	3925
35	UTERU20128560	1956	203..721	3926
	UTERU20132620	1957	330..1007	3927
	UTERU20134830	1958	121..1341	3928
	UTERU20139760	1959	982..1659	3929
	UTERU20140010	1960	42..368	3930
40	UTERU20167570	1961	57..710	3931
	UTERU20168960	1962	317..1468	3932
	UTERU20169020	1963	30..782	3933
	UTERU20173030	1964	1985..>2355	3934
	UTERU20176230	1965	1004..1372	3935
45	UTERU20177150	1966	3..350	3936
	UTERU20181270	1967	153..620	3937
	UTERU20185220	1968	521..1357	3938
	UTERU20188670	1969	231..1886	3939
50	UTERU20188840	1970	1834..2181	3940

[0028] Namely, primers used to synthesize polynucleotides can be designed based on the nucleotide sequences of polynucleotides of the present invention shown in SEQ ID NOs in the above Table 1. When one intends to synthesize full-length cDNAs, an oligo dT primer can be used as the 3'-end primer. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0029] A method to design a primer that enables a specific amplification based on the aimed nucleotide sequence

is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, for example, when the 5'-end primer is designed based on the nucleotide sequence of 5' untranslated region (5'UTR), any part of the 5'-end, which ensures the specificity to the cDNA of interest, can be selected as the primer.

[0030] When synthesizing a full-length cDNA, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' -> 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable conditions (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0031] A template DNA for synthesizing the full-length cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones of the present invention are clones with high probability of completeness in length, which were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the very high fullness ratio by oligo-capping, and [2] assembling the 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction).

[0032] However, the uses of primers designed based on the full-length nucleotide sequences provided by the present invention enable easily obtaining full-length cDNAs without such a special technique.

[0033] The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a nucleotide sequence of novel full-length cDNA. If a full-length nucleotide sequence is provided, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0034] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. A rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, has been reported (Nature, Vol.409, 814-823, 2001), and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the nucleotide sequence which includes the 5'-end of the full-length cDNA clone of the present invention, and thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0035] The polypeptide encoded by the full-length cDNA of the invention can be prepared as a recombinant polypeptide or as a natural polypeptide. For example, the recombinant polypeptide can be prepared by inserting the polynucleotide encoding the polypeptide of the invention into a vector, introducing the vector into an appropriate host cell and purifying the polypeptide expressed within the transformed host cell, as described below. In contrast, the natural polypeptide can be prepared, for example, by utilizing an affinity column to which an antibody against the polypeptide of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, *in vitro* translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the polypeptide of the invention.

[0036] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the polypeptides of the present invention. Using the biological activity possessed by the polypeptide of the invention as an index, it is possible to verify whether or not a particular polypeptide is functionally equivalent to the polypeptide of the invention by examining whether or not the polypeptide has said activity.

[0037] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a polypeptide (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such polypeptides can be generated by spontaneous mutations. The present invention also includes a polypeptide comprising the amino acid sequence shown in Table 1 in which one or more amino acids are substituted, deleted, inserted, and/or added, as long as the polypeptides have the equivalent functions to those of the polypeptides identified in the present Examples described later.

[0038] There are no limitations on the number and sites of amino acid mutations, as long as the polypeptides maintain

the functions thereof. The number of mutations typically corresponds to 30% or less, or 20% or less, or 10% or less, preferably 5% or less, or 3% or less of the total amino acids, more preferably 2% or less or 1% or less of the total amino acids. Alternatively, herein, substitution of one or more amino acids includes substitution of several amino acids. As used herein, the term "several amino acids" means, for example, 5 amino acids, preferably 4 or 3 amino acids, more preferably 2 amino acids, and further preferably 1 amino acid.

[0039] From the viewpoint of maintaining the polypeptide function, it is preferable that a substituted amino acid has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0040] In addition, polypeptides functionally equivalent to the polypeptides of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a polynucleotide highly homologous to the polynucleotide encoding the polypeptide identified in the present Example based on the identified nucleotide sequence (Table 1) or a portion thereof and obtain the functionally equivalent polypeptide from the isolated polynucleotide. The present invention includes polypeptides encoded by the polynucleotides hybridizing with the polynucleotides encoding the polypeptides identified in the present Example, as long as the polypeptides are functionally equivalent to the polypeptides identified in the present Example. Organisms from which the functionally equivalent polypeptides are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0041] Washing conditions of hybridization for the isolation of polynucleotides encoding the functionally equivalent polypeptides are usually "1x SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5x SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1x SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6x SSC, 40% Formamide, 25°C", and the washing at "1x SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C". Even more preferable are those in which the hybridization is done at "6x SSC, 50% Formamide, 37°C", and the washing at "0.1x SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the polynucleotides highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5x SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C".

[0042] One skilled in the art can suitably select various conditions, such as dilution ratios of SSC, formamide concentrations, and temperatures to accomplish a similar stringency.

[0043] However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples. Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0044] The amino acid sequences of polypeptides isolated by using the hybridization techniques usually have high identity to those of the polypeptides of the present invention, which are shown in Table 1. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 1 (a). Furthermore, the present invention encompasses a peptide, or polypeptide comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 1 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0045] As used herein, "percent identity" of amino acid sequences or nucleic acids is determined using the algorithm BLAST of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, for example, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, for example, score = 50, wordlength = 3. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs are used. See <http://www.ncbi.nlm.nih.gov>.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.1-6.4) using primers designed based on the nucleotide sequence (Table 1) or a portion thereof identified in the present Example, it is possible to isolate a polynucleotide fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent polypeptide to a particular polypeptide identified in the present Example based on the isolated polynucleotide fragment.

[0047] The present invention also provides a polynucleotide containing at least 15 nucleotides complementary to a

polynucleotide comprising a nucleotide sequence of SEQ ID NOs shown in Table 1 or the complementary strand thereof. Herein, the term "complementary strand" is defined as one strand of a double strand DNA composed of A:T and G:C base pair to the other strand. Also, "complementary" is defined as not only those completely matching within a continuous region of at least 15 nucleotides, but also having an identity of at least 70%, favorably 80% or higher, more favorably 90% or higher, and most favorably 95% or higher within that region. The identity may be determined using the algorithm described herein.

[0048] Such a polynucleotide includes probes and primers used for the detection and amplification of a polynucleotide encoding the inventive polypeptide. When used as a primer, the polynucleotide usually comprises 15 to 100 bp, and preferably of 15 to 35 bp. When used as a probe, the polynucleotide comprises the whole or a part of the sequence of a polynucleotide of the invention, and comprises at least 15 bp. When used as primers, such polynucleotides are complementary at the 3'-end, and restriction enzyme recognition sequences or tags can be added to the 5'-end.

[0049] Furthermore, polynucleotides of the present invention include an antisense polynucleotide for suppressing the expression of a polypeptide of the invention, which comprises an amino acid sequence of SEQ ID NOs shown in Table 1. To exert an antisense effect, an antisense polynucleotide has at least 15 bp or more, for example 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and usually has 3000 bp or less, and preferably 2000 bp or less. Antisense polynucleotides can be used in the gene therapy of diseases caused by abnormalities of the polypeptides of the invention (abnormal function or abnormal expression). An antisense polynucleotide can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the sequence information of polynucleotide encoding a polypeptide of the invention (for example, the nucleotide sequences of SEQ ID NO: 1 to 1970).

[0050] The polynucleotides or antisense polynucleotides of the present invention can be used in, for example, gene therapy. As target diseases, for example, cancers or various inflammatory diseases may be preferable. These molecules can be used for gene therapy, for example, by administering them to patients by the *in vivo* or *ex vivo* method using virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-related virus vectors, or non-virus vectors such as liposomes.

[0051] The present invention also includes a partial peptide of the polypeptides of the invention. The partial peptide comprises a polypeptide generated as a result that a signal peptide has been removed from a secretory protein. If the polypeptide of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the polypeptide and may bind to the receptor (or ligand). In addition, the present invention includes an antigen peptide for raising antibodies. For the peptides to be specific for the polypeptide of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the polypeptide of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the polypeptide of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the polypeptide of the invention with an appropriate peptidase.

[0052] The present invention also relates to a vector into which a polynucleotide of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted polynucleotide stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the polypeptide of the invention, expression vectors are especially useful. Any expression vector can be used as long as it is capable of expressing the polypeptide *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression. To insert the polynucleotide of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0053] Recently, the technique of GATEWAY™ system (Invitrogen), which is an expression vector construction system for polypeptide expression, has been developed (Experimental Medicine, Vol. 18, No. 19 (December), p2716-2717, 2000). This system includes two types of site-specific recombinases (BP CLONASE™ and LR CLONASE™) derived from lambda phage and uses BP CLONASE™-specific recombination sites for an Entry Vector and LR CLONASE™-specific recombination sites for a Destination Vector, which may comprise a tag useful for polypeptide purification. With this system, an expression vector can be obtained by using homologous recombination.

[0054] First, a polynucleotide fragment of interest is inserted into the entry vector using the first recombination. Then, the secondary recombination is allowed to take place between the entry vector, where the polynucleotide fragment of interest has been inserted, and the destination vector. Thus, the expression vector can be prepared rapidly and highly efficiently. With the above-mentioned typical method using restriction enzyme and ligase reactions, the step of expression vector construction and expression of polypeptide of interest takes about 7 to 10 days. However, with the GATEWAY™ system, the polypeptide of interest can be expressed and prepared in only 3 to 4 days. Thus, the system ensures a high-throughput functional analysis for expressed polypeptides (<http://biotech.nikkeibp.co.jp/netlink/lto/gate->

way/).

[0055] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the polypeptide in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0056] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0057] Further, a polynucleotide containing at least 15 nucleotides comprising a nucleotide sequence of any one of the polynucleotides comprising the nucleotide sequences of SEQ ID NOs shown in Table 1 or the complementary strand thereof can be used not only as a primer for synthesizing full-length cDNAs but also for testing and diagnosing the abnormalities of the polypeptide encoded by the full-length cDNA of the present invention. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the polynucleotide of the invention as a primer, polynucleotide encoding the polypeptide of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or sequencing. Especially, in the case where expression of the mRNA of the present invention varies according to a specific disease, analysis of the amount of expression of the mRNA using the polynucleotide of the present invention as a probe or a primer enables detection and diagnosis of the disease.

[0058] The present invention also relates to antibodies that bind to the polypeptide of the invention. There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to an antigen. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies and chimeric antibodies are also included.

[0059] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the polypeptide expressed in *E. coli*, immunizing mice with the polypeptide, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0060] The antibody binding to the polypeptide of the present invention can be used for purification of the polypeptide of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the polypeptide. Specifically, polypeptides can be extracted, for example, from tissues, blood, or cells, and the polypeptide of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0061] Furthermore, the antibody binding to the polypeptide of the present invention can be utilized for treating the diseases that associates with the polypeptide of the invention. If the antibodies are used for treating patients, human antibodies, humanized antibodies, or chimeric antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human (e.g., see "Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez, M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0062] A cDNA of the present invention encodes, for example, an amino acid sequence of a protein that is predicted to have the following function. The use of the amino acid sequences of the polypeptides encoded by the cDNAs of the present invention enables predicting that the polypeptides have the following functions. It can be predicted, from the results of homology search of SwissProt, GenBank, UniGene, or nr, that these polypeptides have such functions. Specifically, for instance, as shown in Examples, searching for a known gene or polypeptide that is homologous to the partial sequence of the full-length cDNA of the invention (1970 clone) and referring the function of the gene and of the polypeptide encoded by the gene make it possible to predict the function of the polypeptide encoded by the cDNA of the invention. In this way, each of 1078 clones out of the 1970 full-length cDNA clones of the invention was predicted to encode a polypeptide that was classified into the following categories:

Secretory and/or membrane protein (516 clones)
 Glycoprotein-related protein (121 clones)
 Signal transduction-related protein (88 clones)
 Transcription-related protein (143 clones)
 Disease-related protein (331 clones)
 Enzyme and/or metabolism-related protein (219 clones)
 Cell division- and/or cell proliferation-related protein (44 clones)

Cytoskeleton-related protein (80 clones)
 Nuclear protein and/or RNA synthesis-related protein (70 clones)
 Protein synthesis- and/or transport-related protein (20 clones)
 Cellular defense-related protein (10 clones)
 5 Development and/or differentiation-related protein (19 clones)
 DNA- and/or RNA-binding protein (168 clones)
 ATP- and/or GTP-binding protein (93 clones)

10 **[0063]** The functions of the polypeptides encoded by the cDNAs of the present invention can be predicted by assessing the presence of signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, and zinc finger motif, SH3 domain, etc. in the amino acid sequences. The programs, PSORT (Nakai K., and Kanehisa M. (1992) *Genomics* 14: 897-911), SOSUI (Hirokawa T. et al. (1998) *Bioinformatics* 14: 378-379) (Mitsui Knowledge Industry), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) *Biochemistry* 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, 15 a partial amino acid sequence of the polypeptide is fused with another polypeptide such as GFP, the fusion polypeptide is transfected into cultured cells, and the localization is analyzed to predict the function of the original polypeptide.

[0064] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the polypeptides encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot, UniGene, and nr for homologies of the cDNAs; or by searching the 20 amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software programs such as Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) and PROSITE (<http://www.expasy.ch/prosite/>). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using 25 partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus, it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences.

[0065] GenBank, Swiss-Prot, UniGene and nr databases were searched for homologies of the full-length nucleotide sequences of the 1970 clones (see Example 6). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of polypeptides 30 encoded by the clones and the categorization thereof were performed based on these results obtained. The categorization was carried out by the following method.

35 [1] Firstly, the cDNA clones were classified into the above-mentioned 14 functional categories based on the results of annotation-based categorization (using the keywords in the case of Swiss-Prot hit data; using Definition or Reference information in the case of GenBank, UniGene, or nr hit data), and the signal sequence search of the deduced ORFs by PSORT and the transmembrane region search by SOSUI.

40 [2] Secondly, clones which had been unassignable to the categories by the method of [1] were searched for functional domains and/or motifs by Pfam. Based on the results, the clones were additionally classified into the above-mentioned 14 types of categories when they had a functional domain and/or motif assignable to any one of the categories.

[0066] The following 516 clones presumably belong to secretory and/or membrane proteins.

45 ADRGL20020290, ADRGL20021910, ADRGL20036380, ADRGL20036840, ADRGL20059610, ADRGL20063770, ADRGL20066770, ASTRO20010010, ASTRO20020240, ASTRO20045840, ASTRO20053430, ASTRO20055530, ASTRO20055570, ASTRO20055930, ASTRO2008B950, ASTRO20091180, BNGH420021680, BNGH420023870, BNGH420046790, BNGH420052350, BNGH420059680, BNGH420075940, BNGH420077980, BRACE10000510, BRACE20051930, BRACE20052530, BRACE20054080, BRACE20066360, BRACE20068710, BRACE200690
 50 BRACE20069110, BRACE20194670, BRACE20204670, BRACE20216950, BRAMY10001730, BRAMY20003880, BRAMY20013670, BRAMY20024790, BRAMY20027390, BRAMY20028530, BRAMY20035380, BRAMY20044920, BRAMY20045210, BRAMY20047560, BRAMY20050940, BRAMY20053910, BRAMY20055760, BRAMY20072440, BRAMY20083820, BRAMY20089770, BRAMY20091230, BRAMY20094890, BRAMY20096930, BRAMY20118410, BRAMY20123400, BRAMY20125550, BRAMY20127310, BRAMY20127760, BRAMY20135720, BRAMY20137360, BRAMY20139440, BRAMY20152510, BRAMY20194680, BRAMY20204270, BRAMY20225320, BRAMY20237190, 55 BRAMY20245140, BRAMY20251750, BRAMY20285650, BRAWH20020470, BRAWH20021910, BRAWH20026010, BRAWH20030000, BRAWH20039640, BRAWH20055330, BRAWH20078620, BRAWH20093070, BRAWH20185270, BRCAN10000760, BRCAN10001680, BRCAN20001480, BRCAN20004180, BRCAN20005230, BRCOC20000470, BRCOC20003600, BRHIP10000720, BRHIP10001040, BRHIP20000210, BRSSN20001970, BRSSN20074640,

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BRSSN20091190, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20041260, CTONG20044870, CTONG20045500, CTONG20049480, CTONG20051450, CTONG20055850, CTONG20056150, CTONG20059130, CTONG20060040, CTONG20063770, CTONG20065680, CTONG20068360, CTONG20069320, CTONG20071680, CTONG20076810, CTONG20078340, CTONG20079590, CTONG20083980, CTONG20084020, CTONG20085210, 5 CTONG20167750, CTONG20168240, CTONG20179890, CTONG20183830, CTONG20184830, DFNES20018000, DFNES20029660, DFNES20057660, DFNES20072990, DFNES20080880, FCBBF20018680, FCBBF20029280, FCBBF20032930, FCBBF20036360, FCBBF20054390, FCBBF30004340, FCBBF30022680, FCBBF30029250, FCBBF30042610, FCBBF30062490, FCBBF30075970, FCBBF30078600, FCBBF30091520, FCBBF30095410, FCBBF30105440, FCBBF30118670, FCBBF30132660, FCBBF30135890, FCBBF30145670, FCBBF30164510, 10 FCBBF30169870, FCBBF30171230, FCBBF30172330, FCBBF30177290, FCBBF30179740, FCBBF30195690, FCBBF30197840, FCBBF30212210, FCBBF30223110, FCBBF30223210, FCBBF30225930, FCBBF30230610, FCBBF30260480, FCBBF30266510, FCBBF30287940, FCBBF50000610, FCBBF50004950, FEBRA20007820, FEBRA20018670, FEBRA20031280, FEBRA20031810, FEBRA20038220, FEBRA20039260, FEBRA20040230, FEBRA20040560, FEBRA20046280, FEBRA20080860, FEBRA20084750, FEBRA20088810, FEBRA20115930, 15 FEBRA20116650, FEBRA20121950, FEBRA20141980, FEBRA20177800, FEBRA20182030, FEBRA20191720, HCHON10001660, HCHON20015050, HEART10001490, HEART20031680, HHDPC10001140, HHDPC20051850, HHDPC20082790, HHDPC20088160, HLUNG20015070, HLUNG20015180, HLUNG20020850, HLUNG20029490, HLUNG20032460, HLUNG20033350, HLUNG20034970, HLUNG20037160, HLUNG20041540, HLUNG20042730, HLUNG20050760, HLUNG20052300, HLUNG20060670, HLUNG20065990, HLUNG20074330, HLUNG20081390, 20 HLUNG20088750, HLUNG20092530, KIDNE20016360, KIDNE20083150, KIDNE20084030, KIDNE20084040, KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20094670, KIDNE20134130, KIDNE20142900, KIDNE20143200, KIDNE20148080, KIDNE20160960, KIDNE20163710, KIDNE20169180, KIDNE20182540, KIDNE20186170, KIDNE20188630, KIDNE20189960, LIVER20007750, LIVER20010510, LIVER20010990, LIVER20026440, LIVER20030650, LIVER20038000, MESAN20007110, MESAN20008150, MESAN20021220, 25 MESAN20027900, MESAN20058110, MESAN20059570, MESAN20060430, MESAN20067430, MESAN20084150, MESAN20095220, NT2NE20018740, NT2NE20021860, NT2NE20039210, NT2NE20053230, NT2NE20059210, NT2NE20064780, NT2NE20069580, NT2NE20080770, NT2NE20082130, NT2NE20092950, NT2NE20140130, NT2NE20145250, NT2NE20146510, NT2NE20152620, NT2NE20167660, NT2NE20181800, NT2RI20016240, NT2RI20021200, NT2RI20033920, NT2RP70003110, NT2RP70027790, NT2RP70031070, NT2RP70031480, 30 NT2RP70056690, NT2RP70087140, NTONG20034540, NTONG20053630, OCBBF20000740, OCBBF20012520, OCBBF20109780, OCBBF20110210, OCBBF20110730, OCBBF20112280, OCBBF20118720, OCBBF20120010, OCBBF20123200, OCBBF20155030, OCBBF20165900, OCBBF20165910, OCBBF20170350, OCBBF20176650, OCBBF20185630, OCBBF20191950, PANCER10000860, PEBLM20001800, PLACE50001290, PLACE60004260, PLACE60006300, PLACE60053280, PLACE60055590, PLACE60056910, PLACE60057860, PLACE60061370, 35 PLACE60064740, PLACE60070500, PLACE60087680, PLACE60104630, PLACE60107010, PLACE60113340, PLACE60138840, PLACE60154450, PLACE60184870, PROST10001100, PROST20011160, PROST20014150, PROST20035830, PROST20045700, PROST20050390, PROST20065100, PROST20073280, PROST20082430, PROST20084680, PROST20084720, PROST20099090, PROST20105450, PROST20106060, PROST20108850, PROST20110120, PROST20114100, PROST20146590, PROST20152510, PROST20168600, PUAEN10000870, 40 SKMUS20006790, SKMUS20020770, SKMUS20073150, SKMUS20091900, SKNMC20006350, SKNSH20094350, SMINT20006090, SMINT20008110, SMINT20024140, SMINT20028840, SMINT20045470, SMINT20077960, SMINT20081330, SMINT20086250, SMINT20088440, SMINT20088690, SMINT20092160, SPLEN20015100, SPLEN20017610, SPLEN20017810, SPLEN20024190, SPLEN20024620, SPLEN20054500, SPLEN20058180, SPLEN20063890, SPLEN20073880, SPLEN20080070, SPLEN20090880, SPLEN20101950, SPLEN20104690, 45 SPLEN20105100, SPLEN20108000, SPLEN20110180, SPLEN20110860, SPLEN20118050, SPLEN20121790, SPLEN20125230, SPLEN20136700, SPLEN20138600, SPLEN20139100, SPLEN20175920, SPLEN20177400, SPLEN20182850, SPLEN20183020, SPLEN20183950, SPLEN20190080, SPLEN20190770, SPLEN20193230, SPLEN20193490, SPLEN20193790, SPLEN20201830, SPLEN20204670, TESOP10000350, TESTI10000190, TESTI20006160, TESTI20029100, TESTI20031310, TESTI20032770, TESTI20038240, TESTI20043130, 50 TESTI20043220, TESTI20045390, TESTI20046540, TESTI20046870, TESTI20047370, TESTI20050400, TESTI20051200, TESTI20051730, TESTI20053260, TESTI20053780, TESTI20057200, TESTI20057590, TESTI20059080, TESTI20061200, TESTI20062120, TESTI20063330, TESTI20063410, TESTI20063600, TESTI20066330, TESTI20068530, TESTI20070400, TESTI20070740, TESTI20073460, TESTI20086840, TESTI20095200, TESTI20095440, TESTI20095880, TESTI20100090, TESTI20102390, TESTI20105910, 55 TESTI20113940, TESTI20116120, TESTI20121040, TESTI20121710, TESTI20131440, TESTI20142540, TESTI20149880, TESTI20151800, TESTI20162780, TESTI20170170, TESTI20173050, TESTI20182760, TESTI20183680, TESTI20184750, TESTI20186110, TESTI20198540, TESTI20199110, TESTI20202830, TESTI20204260, TESTI20210030, TESTI20214630, TESTI20219110, TESTI20244730, TESTI20245600,

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TESTI20245860, TESTI20246410, TESTI20251610, TESTI20257910, TESTI20260640, TESTI20261040, TESTI20262150, TESTI20262940, TESTI20264910, TESTI20271790, TESTI20278280, TESTI20282420, TESTI20282900, TESTI20286590, THYMU20007020, THYMU20012020, THYMU20017270, THYMU20020800, THYMU20025480, THYMU20028150, THYMU20030690, THYMU20034790, THYMU20046350, THYMU20046770, THYMU20050010, THYMU20052830, THYMU20054800, THYMU20055740, THYMU20055760, THYMU20062770, THYMU20078240, THYMU20079690, THYMU20083390, THYMU20087270, THYMU20100940, THYMU20115380, THYMU20137050, THYMU20137570, THYMU20143230, THYMU20150190, THYMU20153210, THYMU20154790, THYMU20163600, THYMU20171580, THYMU20178440, THYMU20185470, TRACH20011010, TRACH20011540, TRACH20021380, TRACH20073990, TRACH20081270, TRACH20090060, TRACH20149720, TRACH20149740, TRACH20159390, TRACH20163470, TRACH20165330, TRACH20167090, TRACH20173680, TRACH20190460, UMVEN10001380, UTERU20035770, UTERU20040150, UTERU20045200, UTERU20064120, UTERU20086530, UTERU20087070, UTERU20087850, UTERU20089300, UTERU20089620, UTERU20095100, UTERU20099040, UTERU20103200, UTERU20125810, UTERU20127030, UTERU20127150, UTERU20139760, UTERU20188840

[0067] The following 121 clones presumably belong to glycoprotein-related proteins.

ADRL20020290, ADRL20036840, ADRL20059610, ADRL20066770, ASTRO20055570, BNGH420046790, BNGH420077980, BRACE20051930, BRACE20069000, BRACE20204670, BRACE20216950, BRAMY20013670, BRAMY20089770, BRAMY20251210, BRAWH20039640, BRCAN10000760, BRCAN20005230, BRCOC20003600, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20045500, CTONG20059130, CTONG20079590, CTONG20085210, CTONG20184830, DFNES20018000, DFNES20080880, FCBBF30004340, FCBBF30029250, FCBBF30062490, FCBBF30091520, FCBBF30164510, FCBBF30171230, FCBBF30195690, FCBBF30223210, FEBRA20038220, HCHON20015050, HLUNG20015070, HLUNG20032460, HLUNG20037160, HLUNG20041540, KIDNE20142900, KIDNE20169180, KIDNE20186170, KIDNE20189960, MESAN20021220, MESAN20058110, NT2NE20064780, NT2NE20140130, NT2NE20155650, NT2RP70056690, NTONG20053630, OCBBF20000740, OCBBF20012520, OCBBF20110210, OCBBF20120010, OCBBF20165900, OCBBF20165910, OCBBF20191950, PEBLM20001800, PLACE60004260, PLACE60087680, PLACE60113340, PLACE60184870, PROST20033240, PROST20099090, PROST20108850, PROST20146590, SKMUS20073150, SKNMC20006350, SMINT20028840, SMINT20056230, SMINT20083290, SMINT20091190, SPLEN20024620, SPLEN20063890, SPLEN20080070, SPLEN20090880, SPLEN20118050, SPLEN20139100, SPLEN20183020, SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20043990, TESTI20045390, TESTI20051200, TESTI20057590, TESTI20059080, TESTI20066330, TESTI20086840, TESTI20100090, TESTI20105910, TESTI20154370, TESTI20164210, TESTI20182760, TESTI20184750, TESTI20199110, TESTI20219110, TESTI20220230, TESTI20245600, TESTI20251610, TESTI20257910, TESTI20286590, THYMU20024500, THYMU20028150, THYMU20052830, THYMU20062770, THYMU20099060, THYMU20170080, THYMU20178440, TRACH20011010, TRACH20011540, TRACH20021380, TRACH20149740, TRACH20170860, TRACH20190460, UTERU20086530, UTERU20087070, UTERU20127030

[0068] The following 88 clones presumably belong to signal transduction-related proteins.

ASTRO20050810, ASTRO20052420, ASTRO20085080, ASTRO20090680, BNGH420008150, BNGH420015760, BNGH420035290, BNGH420086030, BRAMY20035830, BRAMY20043630, BRAMY20118490, BRAMY20206340, BRAMY20244490, BRAMY20251210, BRAMY20263000, BRAWH20093040, BRAWH20190550, CTONG20004520, CTONG20029030, CTONG20030280, CTONG20063930, CTONG20070720, CTONG20189000, FCBBF30001100, FCBBF30076310, FCBBF30100080, FCBBF30143550, FCBBF30153170, FCBBF30175350, FCBBF30250980, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, HLUNG20084790, KIDNE20089870, KIDNE20160360, LIVER20011640, MESAN20021130, MESAN20027240, MESAN20065990, NT2NE20018890, NT2NE20042550, NT2RP70075800, NTONG20043080, NTONG20048440, PLACE60071800, PROST20033240, PROST20052850, PROST20065790, PROST20075280, SKNSH20052400, SKNSH20057920, SMINT20006020, SMINT20035050, SPLEN20023540, SPLEN20039180, SPLEN20048800, SPLEN20049840, SPLEN20054160, SPLEN20085910, SPLEN20191020, SPLEN20198390, TESTI20046490, TESTI20049060, TESTI20053070, TESTI20066650, TESTI20081890, TESTI20095770, TESTI20106820, TESTI20112860, TESTI20145780, TESTI20150420, TESTI20168880, TESTI20205250, TESTI20228120, TESTI20244220, TESTI20244460, TESTI20251740, TESTI20261160, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20106990, THYMU20145990, THYMU20170080, THYMU20176010, TRACH20188350

[0069] The following 143 clones presumably belong to transcription-related proteins.

ASTRO20038400, ASTRO20075150, BNGH420070370, BNGH420074600, BNGH420087430, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAWH20040680, BRAWH20050740, BRAWH20080580, BRAWH20082920, BRAWH20095900, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20084660, CTONG20186370, CTONG20186520, DFNES20028170, DFNES20046840, DFNES20073320, FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30093170, FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30143550,

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FCBBF30220050, FCBBF30228940, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20170240, HCHON10000150, HCHON20002650, HEART20019310, HLUNG20014590, HLUNG20028110, HLUNG2006370, KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20038520, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20061030, NT2NE20079670, NT2NE20082600, NT2RP70001120, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450, OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM20003260, PLACE60052940, PLACE60066970, PLACE60122970, PLACE60150510, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20127450, PROST20151370, PROST20155370, PUAEN10000650, PUAEN20003120, SMINT20011950, SMINT20026200, SMINT20030740, SMINT20039050, SMINT20044140, SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20098030, SPLEN20197930, TESTI10001570, TESTI20057430, TESTI20057840, TESTI20059810, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20122070, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20194880, TESTI20197600, TESTI20228740, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20274960, TESTI20282530, THYMU10004280, THYMU20019260, THYMU20032820, THYMU20071120, THYMU20077250, TKIDN10001920, UTERU20016580, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20185220, UTERU20188670
[0070] The following 331 clones presumably belong to disease-related proteins.
 ADRGL20020290, ADRGL20021910, ADRGL20026790, ADRGL20036840, ADRGL20059610, ADRGL20066770, ASTRO20038400, ASTRO20052420, ASTRO20055570, ASTRO20075150, ASTRO20088950, BNGH420008150, BNGH420086030, BRACE10000510, BRACE20003310, BRACE20069000, BRACE20097540, BRACE20194670, BRACE20196180, BRACE20204670, BRACE20216950, BRAMY20003540, BRAMY20005080, BRAMY20035830, BRAMY20040580, BRAMY20043630, BRAMY20044920, BRAMY20051820, BRAMY20056620, BRAMY20089770, BRAMY20111780, BRAMY20152510, BRAMY20190550, BRAMY20221600, BRAMY20227860, BRAMY20274510, BRAWH20082920, BRAWH20093040, BRAWH20095900, BRAWH20190530, BRAWH20191980, BRCAN10000760, BRCAN10001050, BRCAN20005230, BRSSN20066440, CTONG20004520, CTONG20029030, CTONG20042640, CTONG20045500, CTONG20052780, CTONG20053990, CTONG20070780, CTONG20070910, CTONG20072930, CTONG20083980, CTONG20084660, CTONG20165750, CTONG20169040, CTONG20183430, CTONG20183830, CTONG20186290, CTONG20189000, DFNES20016470, DFNES20025500, DFNES20046840, DFNES20055400, DFNES20080880, FCBBF10000230, FCBBF20035490, FCBBF20066340, FCBBF30002270, FCBBF30002280, FCBBF30019140, FCBBF30053300, FCBBF30071500, FCBBF30072440, FCBBF30076310, FCBBF30080730, FCBBF30100080, FCBBF30115920, FCBBF30118670, FCBBF30129010, FCBBF30132050, FCBBF30136230, FCBBF30153170, FCBBF30164510, FCBBF30166220, FCBBF30171230, FCBBF30175350, FCBBF30194550, FCBBF30220050, FCBBF30223210, FCBBF30259050, FCBBF30263080, FCBBF30275590, FCBBF50001650, FEBRA20027070, FEBRA20045380, FEBRA20046200, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20078800, FEBRA20087550, FEBRA20088810, FEBRA20090160, FEBRA20092760, FEBRA20151750, FEBRA20170240, FEBRA20173330, FEBRA20191720, HCHON10000150, HCHON20015050, HEART20009590, HEART20022200, HEART20063100, HHDP20081230, HLUNG20008460, HLUNG20014590, HLUNG20032460, HLUNG20063700, HLUNG20065990, HLUNG20069350, HLUNG20081530, HLUNG20082350, HLUNG20083330, HLUNG20085210, KIDNE20081170, KIDNE20084040, KIDNE20088240, KIDNE20089870, KIDNE20133460, KIDNE20134890, KIDNE20141700, KIDNE20142900, KIDNE20150730, KIDNE20152440, KIDNE20160360, KIDNE20165390, KIDNE20169180, KIDNE20173430, KIDNE20189960, LIVER20026440, MESAN20006200, MESAN20021130, MESAN20033220, MESAN20056890, MESAN20057240, MESAN20065990, MESAN20067430, MESAN20069530, NESOP20004520, NT2NE20018890, NT2NE20026200, NT2NE20037050, NT2NE20053950, NT2NE20061030, NT2NE20111190, NT2NE20117580, NT2NE20119980, NT2NE20140130, NT2NE20141040, NT2RI20093010, NT2RP70003110, NT2RP70046410, NT2RP70075300, NTONG20032100, NTONG20034540, OCBBF20000740, OCBBF20012520, OCBBF20111600, OCBBF20120010, OCBBF20156450, OCBBF20157970, OCBBF20191950, PEBLM20001800, PEBLM20003260, PLACE60004260, PLACE6001262, PLACE60054230, PLACE60054870, PLACE60062660, PLACE60087680, PLACE60184870, PROST20015210, PROST20024250, PROST20036350, PROST20050390, PROST20058860, PROST20063430, PROST20065790, PROST20084720, PROST20099090, PROST20120070, PROST20127450, PROST20146590, PROST20152510, PROST20168600, PUAEN10000650, PUAEN20003120, SKMUS20008730, SKMUS20017400, SKMUS20040440, SKMUS20073590, SKMUS20079150, SKNSH20009710, SMINT20002320, SMINT20007470, SMINT20008110, SMINT20011950, SMINT20016150, SMINT20026200, SMINT20030740, SMINT20049920, SMINT20077960, SMINT20083290, SMINT20086250, SMINT20089600, SMINT20091190, SPLEN20023540, SPLEN20024190, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20057830, SPLEN20059270, SPLEN20063890, SPLEN20073500, SPLEN20080070, SPLEN20085910, SPLEN20090880, SPLEN20098030, SPLEN20118050, SPLEN20136730,

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SPLEN20138600, SPLEN20139100, SPLEN20139360, SPLEN20180980, SPLEN20187490, SPLEN20193790,
 SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20035790, TESTI20041630, TESTI20049060,
 TESTI20050720, TESTI20051200, TESTI20057430, TESTI20057590, TESTI20059080, TESTI20062120,
 TESTI20067480, TESTI20071630, TESTI20099350, TESTI20105130, TESTI20105910, TESTI20108060,
 5 TESTI20125920, TESTI20130530, TESTI20131440, TESTI20134680, TESTI20142540, TESTI20143180,
 TESTI20150420, TESTI20154370, TESTI20164210, TESTI20166670, TESTI20168880, TESTI20171070,
 TESTI20182760, TESTI20184750, TESTI20193080, TESTI20194880, TESTI20196970, TESTI20197600,
 TESTI20201760, TESTI20207170, TESTI20219110, TESTI20228740, TESTI20244430, TESTI20246480,
 TESTI20251740, TESTI20252690, TESTI20254030, TESTI20257910, TESTI20258720, TESTI20266050,
 10 TESTI20271790, TESTI20274960, TESTI20282530, TESTI20286590, THYMU10004280, THYMU20006020,
 THYMU20013250, THYMU20019260, THYMU20023560, THYMU20028150, THYMU20032820, THYMU20034400,
 THYMU20055460, THYMU20063650, THYMU20070250, THYMU20071120, THYMU20081110, THYMU20090230,
 THYMU20095920, THYMU20098350, THYMU20099060, THYMU20120730, THYMU20121040, THYMU20170080,
 THYMU20185650, THYMU20191970, TKIDN10000620, TKIDN10001920, TRACH20011540, TRACH20091070,
 15 TRACH20143710, TRACH20170860, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20086530,
 UTERU20087070, UTERU20087850, UTERU20099510, UTERU20101150, UTERU20104310, UTERU20127030,
 UTERU20185220

[0071] The following 219 clones presumably belong to the category of enzymes and/or metabolism-related proteins.

20 ADRGL20059610, ASTRO20026320, ASTRO20050810, ASTRO20088950, BNGH420008150, BNGH420035290,
 BNGH420074600, BRACE20050870, BRACE20097540, BRACE20200770, BRACE20204670, BRACE20215410,
 BRAMY20003540, BRAMY20005080, BRAMY20027990, BRAMY20028620, BRAMY20044920, BRAMY20055760,
 BRAMY20056620, BRAMY20072870, BRAMY20093490, BRAMY20096930, BRAMY20118490, BRAMY20125360,
 BRAMY20143870, BRAMY20152510, BRAMY20231150, BRAMY20244490, BRAMY20251210, BRAWH20021910,
 BRAWH20082920, BRAWH20093040, BRAWH20094900, BRAWH20183170, BRAWH20188750, BRAWH20190550,
 25 BRAWH20191980, BRCAN20005230, BRCOC20003600, CTONG20051100, CTONG20070910, CTONG20076810,
 CTONG20079590, CTONG20080140, CTONG20085210, CTONG20186290, DFNES20063460, DFNES20080880,
 FCBBF20023490, FCBBF20066340, FCBBF30004340, FCBBF30019140, FCBBF30022680, FCBBF30029250,
 FCBBF30072440, FCBBF30076310, FCBBF30085560, FCBBF30091520, FCBBF30107290, FCBBF30125880,
 FCBBF30132050, FCBBF30143550, FCBBF30153170, FCBBF30166220, FCBBF30171230, FCBBF30175350,
 30 FCBBF30236670, FCBBF30260480, FEBRA20038220, FEBRA20040560, FEBRA20078800, FEBRA20090160,
 FEBRA20172230, FEBRA20173330, HCHON20000870, HCHON20002710, HEART10001490, HEART20042730,
 HEART20047640, HEART20082570, HLUNG20011260, HLUNG20032460, HLUNG20041540, HLUNG20042730,
 HLUNG20054790, KIDNE20080690, KIDNE20083620, KIDNE20084040, KIDNE20147170, KIDNE20152440,
 KIDNE20173150, KIDNE20186170, KIDNE20189960, LIVER20011640, LIVER20026440, LIVER20055270,
 35 MESAN20021130, MESAN20033220, MESAN20038520, MESAN20057240, MESAN20058110, MESAN20065990,
 MESAN20095800, NT2NE20026200, NT2NE20042550, NT2NE20117580, NT2NE20127900, NT2RI20093010,
 NT2RP70064570, NTONG20034540, NTONG20043080, NTONG20053630, NTONG20053730, NTONG20058010,
 OCBFF20120010, OCBFF20167290, OCBFF20191950, PANC10000860, PLACE60052940, PLACE60064180,
 PLACE60073090, PLACE60095600, PLACE60184410, PLACE60188630, PROST20007600, PROST20033240,
 40 PROST20036350, PROST20039300, PROST20050390, PROST20051310, PROST20052850, PROST20065790,
 PROST20075280, PROST20084720, PROST20099090, PROST20108850, PROST20152510, PUAEN20001520,
 PUAEN20002470, SKNMC20006350, SKNSH20057920, SMINT20008110, SMINT20049920, SMINT20094680,
 SPLEN20023540, SPLEN20024930, SPLEN20043680, SPLEN20048800, SPLEN20054500, SPLEN20057900,
 SPLEN20071820, SPLEN20080070, SPLEN20085910, SPLEN20108000, SPLEN20136730, SPLEN20180980,
 45 TESTI20012080, TESTI20030200, TESTI20031310, TESTI20038240, TESTI20050720, TESTI20051200,
 TESTI20059080, TESTI20062120, TESTI20066330, TESTI20076570, TESTI20103690, TESTI20105130,
 TESTI20106820, TESTI20108060, TESTI20112860, TESTI20121040, TESTI20130530, TESTI20131440,
 TESTI20168880, TESTI20170170, TESTI20196690, TESTI20196970, TESTI20199110, TESTI20205250,
 TESTI20212970, TESTI20222030, TESTI20226520, TESTI20227380, TESTI20244460, TESTI20244730,
 50 TESTI20250630, TESTI20260640, TESTI20262940, TESTI20264530, TESTI20285230, THYMU20006020,
 THYMU20013250, THYMU20034400, THYMU20039320, THYMU20055460, THYMU20055760, THYMU20063650,
 THYMU20066660, THYMU20070250, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20110720,
 THYMU20120240, THYMU20120730, THYMU20170230, TRACH20011010, TRACH20021380, TRACH20091070,
 TRACH20113020, TRACH20143710, TRACH20164100, TRACH20190460, UTERU20087070, UTERU20089620,
 55 UTERU20104310, UTERU20185220, UTERU20188670

[0072] The following 44 clones presumably belong to the category of cell division- and/or cell proliferation-related proteins.

ASTRO20090680, BRACE20079370, BRAMY20234820, BRCAN10001050, BRCAN20005410, CTONG20032930,

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FCBBF20070950, FCBBF30002270, FCBBF30053300, FCBBF30105860, FCBBF30175350, FCBBF30215240, FCBBF30275590, FEBRA20045380, HLUNG20068120, KIDNE20134890, KIDNE20150730, MESAN20021470, NT2NE20077250, NT2NE20153620, NT2RP70030840, NTONG20053910, OCBBF20111370, OCBBF20174580, PROST20063430, SKNMC10001230, SMINT20028800, SPLEN20023540, SPLEN20057830, SPLEN20139360, TESTI20031410, TESTI20057840, TESTI20065650, TESTI20066650, TESTI20107320, TESTI20108060, TESTI20114480, TESTI20134680, TESTI2014318 TESTI20150920, TESTI20201760, TESTI20278280, TESTI20284260, THYMU20097920

[0073] The following 80 clones presumably belong to the category of cytoskeleton-related proteins.

ADRL20062330, ASTRO20053430, BGGI120000670, BRACE20079370, BRAMY20038980, BRAMY20083330, BRAMY20094890, CTONG20004110, CTONG20032930, CTONG20077760, CTONG20083980, CTONG20169040, CTONG20183430, DFNES20018000, FCBBF30105860, FCBBF30130410, FCBBF30194550, FCBBF30201630, FCBBF30271990, FEBRA20005040, FEBRA20046200, FEBRA20099860, HCHON20015050, HLUNG20081530, KIDNE20081170, NT2RP70001730, NT2RP70003110, NTONG20032100, OCBBF20166890, OCBBF20174890, PLACE60054870, PLACE60055590, PLACE60071800, PLACE60118810, PROST20015210, PROST20097840, PROST20120070, PROST20146590, SKMUS20007260, SKMUS20008730, SKMUS20017400, SKMUS20073590, SMINT20062050, SMINT20074330, SMINT20077960, SPLEN20039180, SPLEN20049840, SPLEN20076470, SPLEN20182990, SPLEN20187490, SPLEN20195710, TESTI10000190, TESTI20041630, TESTI20057880, TESTI20058920, TESTI20060080, TESTI20064530, TESTI20064650, TESTI20065650, TESTI20067440, TESTI20071130, TESTI20099350, TESTI20112540, TESTI20125280, TESTI20136010, TESTI20153310, TESTI20175370, TESTI2022460, TESTI20244430, TESTI20254030, TESTI20258720, THYMU20024500, THYMU20062610, THYMU20098350, TRACH20043360, TRACH20098510, TRACH20149500, UTERU20089390, UTERU20122520, UTERU20168960

[0074] The following 70 clones presumably belong to the category of nuclear proteins and/or RNA synthesis-related proteins.

ASTRO20026320, BRACE20050870, BRACE20200770, BRAMY20134050, BRAWH20063010, BRAWH20093040, BRAWH20174330, BRAWH20176850, CTONG20042640, FCBBF20023490, FCBBF20035490, FCBBF20070950, FCBBF30002270, FCBBF30048420, FCBBF30080730, FCBBF30115920, FCBBF30236670, FEBRA20035240, FEBRA20092760, FEBRA20173330, HHDP20081230, HLUNG20011460, HLUNG20068120, KIDNE20089870, KIDNE20150730, MESAN20056890, MESAN20057240, NT2NE20037050, NT2NE20167660, NT2RP70031070, NTONG20053730, PLACE60064180, PLACE60095600, PROST20016760, PROST20051310, PROST20058860, PROST20152510, PUAEN20002470, SKMUS20079150, SKNSH20030640, SPLEN20023850, SPLEN20057830, SPLEN20139360, SPLEN20190430, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20062120, TESTI20065650, TESTI20081890, TESTI20150920, TESTI20153310, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20251740, TESTI20256560, TESTI20260640, TESTI20270130, TESTI20284260, TESTI20285230, THYMU20021090, THYMU20049060, THYMU20066660, THYMU20081110, THYMU20090230, THYMU20120240, UTERU10001060, UTERU20104310

[0075] The following 20 clones presumably belong to the category of protein synthesis- and/or protein transport-related proteins.

BRAMY20038980, BRAMY20274510, CTONG20008190, CTONG20033610, FCBBF20018680, FEBRA20090220, KIDNE20141700, NT2NE20167660, NTONG20055200, PLACE60012620, PROST20036350, PROST20062820, SKMUS20040440, SMINT20000070, SPLEN20180980, TESTI20055680, TESTI20067440, TESTI20107240, THYMU20096580, THYMU20121040

[0076] The following 10 clones presumably belong to the category of cellular defense-related proteins.

ASTRO20089600, BRAMY20117670, FEBRA20087550, HLUNG20081390, MESAN20057240, NTONG20031580, PROST20007600, SPLEN20023850, SPLEN20043680, TESTI20261680

[0077] The following 19 clones presumably belong to the category of development and/or differentiation-related proteins.

BRACE20061620, BRACE20200770, BRAMY20013670, CTONG20017490, CTONG20020950, HCHON10000150, MESAN20021470, OCBBF20165910, PROST20155370, PUAEN20002470, TESTI20079220, TESTI20079980, TESTI20166670, TESTI20184760, TESTI20252690, TRACH20040390, UTERU20089620, UTERU20094830, UTERU20169020

[0078] The following 168 clones presumably belong to the category of DNA- and/or RNA-binding proteins.

ASTRO20038400, BGGI120010750, BNGH420070370, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAMY20274510, BRAWH20040680, BRAWH20050740, BRAWH20063010, BRAWH20080580, BRAWH20095900, BRAWH20174330, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20165750, CTONG20186370, CTONG20186520, DFNES20046840, DFNES20073320, FCBBF20035430, FCBBF20070950, FCBBF30002270, FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30048420, FCBBF30080730, FCBBF30093170,

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FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30220050, FCBBF30228940, FCBBF30236670, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20035240, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20087550, FEBRA20092760, FEBRA20170240, FEBRA20177800, HCHON20002650, HEART20019310, HEART20063100, HHDPC20081230, HLUNG20011460, HLUNG20014590, HLUNG20028110, HLUNG20063700, HLUNG20068120, KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20056890, MESAN20057240, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20079670, NT2NE20082600, NT2NE20087270, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450, OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM10001470, PEBLM20003260, PLACE60066970, PLACE60122970, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20051310, PROST20058860, PROST20151370, PROST20155370, PUAEN20003120, SMINT20011950, SMINT20030740, SMINT20039050, SMINT20044140, SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20139360, SPLEN20190430, TESTI10001570, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20057430, TESTI20059810, TESTI20062120, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20134970, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20197600, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20228740, TESTI20246480, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20268240, TESTI20270130, TESTI20274960, TESTI20282530, TESTI20284260, TESTI20285230, THYMU10004280, THYMU20019260, THYMU20023560, THYMU20032820, THYMU20049060, THYMU20066660, THYMU20071120, THYMU20077250, THYMU20081110, THYMU20090230, TKIDN10001920, TRACH20108240, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20188670

[0079] The following 93 clones presumably belong to the category of ATP- and/or GTP-binding proteins.

ASTRO20026320, BNGH420035290, BRACE20050870, BRACE20079370, BRACE20200770, BRAMY20055760, BRAMY20118490, BRAMY20244490, BRAMY20251210, BRAWH20093040, BRAWH20190550, BRCAN10001050, BRCOC20003600, CTONG20008190, CTONG20030280, CTONG20032930, CTONG20176040, CTONG20184830, FCBBF20023490, FCBBF30019140, FCBBF30076310, FCBBF30105860, FCBBF30175350, FCBBF30201630, FCBBF30236670, FEBRA20005040, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, HLUNG20052300, KIDNE20081170, KIDNE20134890, LIVER20030650, LIVER20055270, MESAN20065990, NT2NE20042550, NTONG20043080, NTONG20055200, OCBBF20182060, PLACE60054870, PLACE60064180, PLACE60095600, PLACE60140640, PROST20015210, PROST20033240, PROST20036350, PROST20051310, PROST20052850, PROST20062820, PROST20075280, PROST20120070, PUAEN20002470, SKNSH20052400, SKNSH20057920, SMINT20008110, SPLEN20023850, SPLEN20043680, SPLEN20049840, SPLEN20136730, SPLEN20180980, SPLEN20193790, TESTI20055680, TESTI20058920, TESTI20060080, TESTI20064650, TESTI20071130, TESTI20099350, TESTI20106820, TESTI20112860, TESTI20134680, TESTI20136010, TESTI20143180, TESTI20175370, TESTI20212970, TESTI20222460, TESTI20227380, TESTI20244220, TESTI20244460, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20062610, THYMU20066660, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20176010, TRACH20043360, TRACH20098510, TRACH20113020, UTERU20185220, UTERU20188670

[0080] Among the clones other than the ones shown above, BNGH420036410, FCBBF30257370 are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

SMINT20044730, TESTI20140970

[0081] The two clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20055560, CTONG20046690, DFNES20043710, FCBBF30005500, MESAN20030350, MESAN20030370, PLACE60074820, TESTI20058350, TESTI20106170, TRACH20131230, UTERU20000950

[0082] The 11 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

ASTRO20010290, BRACE20099070, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20184550

[0083] The 18 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

ADRGL20047770, ADRGL20079060, BRACE20014450, BRACE20051600, BRAWH20185260, CTONG20033750, CTONG20070090, CTONG20190290, FCBBF20020440, FCBBF30005360, FCBBF30173960, FEBRA20031000, KIDNE20087880, LIVER20013890, MESAN20030350, MESAN20030370, OCBBF20113110, PLACE60074820, PLACE60093380, PROST20028970, PROST20102190, SALGL10001070, SPLEN20006950, SPLEN20011350,

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SPLEN20050090, TESTI20060830, TESTI20066150, TESTI20120900, TESTI20132310, TESTI20148380, TESTI20162980, TESTI20166290, TESTI20205100, THYMU20112590, TRACH20029880

[0084] The 35 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

5 PLACE60054820, TESTI20197030

[0085] The two clones shown above are clones which were predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

ASTRO20006530, OCBBF20016390, TRACH20058000

10 **[0086]** The three clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

BRACE20065470, PLACE60054820

[0087] The two clones shown above are clones which were predicted to highly possibly belong to the category of nuclear protein and/or RNA synthesis-related protein based on the result of domain search by Pfam.

15 ASTRO20010290, BRACE20099070, BRAWH20014590, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, MESAN20034440, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20104480, THYMU20184550

[0088] The 21 clones shown above are clones which were predicted to highly possibly belong to the category of DNA- and/or RNA-binding protein based on the result of domain search by Pfam.

20 KIDNE20133880, MESAN20030350, MESAN20030370, TESTI20059480

[0089] The four clones shown above are clones which were predicted to highly possibly belong to the category of ATP- and/or GTP-binding proteins based on the result of domain search by Pfam.

25 **[0090]** The 205 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search using their full-length nucleotide sequences and motif search in their estimated ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (/), are shown below.

ADRL20022600//DIAPHANOUS PROTEIN HOMOLOG 1 (P140MDIA).

ADRL20023920//ABC1 PROTEIN HOMOLOG PRECURSOR.

30 ASTR020001910//Rattus norvegicus mRNA for annexin V-binding protein (ABP-10), partial cds.

ASTR020009140//PUTATIVE COMPETENCE-DAMAGE PROTEIN.

ASTR020046280//PSU1 PROTEIN.

ASTR020058960//DNA damage inducible protein homolog - fission yeast (*Schizosaccharomyces pombe*)

BNGH420024870//C2 domain// C2 domain// C2 domain

BRACE20007330//RING CANAL PROTEIN (KELCH PROTEIN).

35 BRACE20052430//Homo sapiens AMSH mRNA, complete cds.

BRACE20054600//Xenopus laevis mRNA for Kielin, complete cds.

BRACE20059810//TSC-22/dip/bun family

BRACE20063540//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).

BRACE20079200//Xenopus laevis mRNA for Kielin, complete cds.

40 BRAMY20016780//Protein convertase P-domain

BRAMY20023640//UBX domain

BRAMY20045420//Domain found in Dishevelled, Egl-10, and Pleckstrin

BRAMY20056840//UBE-1c2

BRAMY20063750//Homo sapiens HRIHFB2007 mRNA, partial cds.

45 BRAMY20102900//Homo sapiens RU1 (RU1) mRNA, complete cds.

BRAMY20158550//CALMODULIN.

BRAMY20223010//Mus musculus leucine-rich glioma-inactivated 1 protein precursor, (Lgi1) mRNA, complete cds.

BRAMY20238630//TETRATRICOPOLYPEPTIDE REPEAT PROTEIN 4.

BRAMY20245760//Araneus diadematus fibroin-4 mRNA, partial cds.

50 BRAWH20047790//HMG (high mobility group) box

BRSSN20005610//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.

BRSSN20005660//Bacterial type II secretion system protein

BRSSN20093890//Homo sapiens mRNA for Kelch motif containing protein, complete cds.

55 CTONG20041150//Streptomyces ansochromogenes strain 7100 SanE (sanE) gene, complete cds.

CTONG20066110//Homo sapiens DME-6 mRNA, partial cds.

CTONG20069420//Ribosomal protein S14p/S29e

CTONG20071040//BETA CRYSTALLIN B2 (BP).

- CTONG20074170//DENN (AEX-3) domain
 CTONG20083430//Nuclear transition protein 2
 CTONG20170940//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
 CTONG20174290//TRICHOHYALIN.
- 5 CTONG20174580//Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein complete cds.
 CTONG20180690//Collagen triple helix repeat (20 copies)
 CTONG20186550//cca3 protein - rat
 CTONG20188080//TPR Domain
 FCBBF10004760//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
- 10 FCBBF20033360//RING CANAL PROTEIN (KELCH PROTEIN).
 FCBBF20041380//SAM domain (Sterile alpha motif)
 FCBBF20043730//UBA domain
 FCBBF20056580//Mus musculus NSD1 protein mRNA, complete cds.
 FCBBF20059660//TPR Domain
- 15 FCBBF30019180//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY
 SUBUNIT A, ALPHA ISOFORM (PP2A, SUBUNIT A, PR65-ALPHA ISOFORM) (PP2A, SUBUNIT A, R1-ALPHA ISO-
 FORM).
 FCBBF30026580//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.
 FCBBF30035570//C2 domain
- 20 FCBBF30079770//D-isomer specific 2-hydroxyacid dehydrogenases
 FCBBF30100120//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete
 cds.
 FCBBF30100410//Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.
 FCBBF30118890//Drosophila melanogaster La related protein (Iarp) mRNA, partial cds.
- 25 FCBBF30138000//trg protein - rat
 FCBBF30157270//Rattus norvegicus PAPIN mRNA, complete cds.
 FCBBF30161780//gag gene protein p24 (core nucleocapsid protein)// Zinc knuckle
 FCBBF30198670//dof protein - fruit fly (Drosophila melanogaster)
 FCBBF30222910//Mus musculus Rap2 interacting protein 8 (RPIP8) mRNA, complete cds.
- 30 FCBBF30255680//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.
 FCBBF30260210//Drosophila melanogaster KISMET-L long isoform (kis) mRNA, complete cds.
 FCBBF30282020//cca3 protein - rat
 FCBBF40000610//late gestation lung 2 protein [Rattus norvegicus].
 FEBRA20029620//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
- 35 FEBRA20031150//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
 FEBRA20038330//Corticotropin-releasing factor family
 FEBRA20038970//Homo sapiens mRNA for stabilin-1 (stab1 gene).
 FEBRA20088610//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).
 FEBRA20150420//HYPOTHETICAL 131.5 KDA PROTEIN C02F12.7 IN CHROMOSOME X.
- 40 FEBRA20175330//D-isomer specific 2-hydroxyacid dehydrogenases
 HEART10001420//Mus musculus skm-BOP1 (Bop) mRNA, complete cds.
 HLUNG20024050//Rubredoxin
 HLUNG20030420//Mus musculus mRNA for MAIL, complete cds.
 HLUNG20030490//Ambystoma tigrinum RPE65 protein mRNA, complete cds.
- 45 HLUNG20033060//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
 HLUNG20041590//ubiquitous tetratricopeptide containing protein RoXaN [Homo sapiens].
 HLUNG20045340//MOB2 PROTEIN (MPS1 BINDER 2).
 HLUNG20051330//FHIPEP family
 HLUNG20070410//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
- 50 HLUNG20072100//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds.
 HLUNG20083480//Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52.
 KIDNE20027980//SAM domain (Sterile alpha motif)
 KIDNE20084730//Homo sapiens FH1/FH2 domain-containing protein FHOS (FHOS) mRNA, complete cds.
 KIDNE20149780//NG28 [Mus musculus]
- 55 KIDNE20154330//Rattus norvegicus mRNA for multi PDZ domain protein.
 KIDNE20170400//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Protein kinase C terminal do-
 main// Rubredoxin
 KIDNE20189890//Homo sapiens mRNA for KARP-1-binding protein 2 (KAB2), complete cds.

- LIVER20010760//Homo sapiens C-type lectin-like receptor-1 mRNA, complete cds.
 LIVER20040740//RETINAL-BINDING PROTEIN (RALBP).
 MESAN20009090//Homo sapiens CEGP1 protein (CEGP1), mRNA
 MESAN20026870//PAN domain// TBC domain
 5 MESAN20090190//CEGP1 protein [Homo sapiens].
 NT2NE20059680//Homo sapiens integrin cytoplasmic domain associated protein (Icap-1a) mRNA, complete cds.
 NT2NE20077270//Adenovirus EB1 55K protein / large t-antigen
 NT2NE20087850//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
 NT2NE20095230//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
 10 NT2NE20108420//KES1 PROTEIN.
 NT2NE20173970//Rattus norvegicus beta-catenin binding protein mRNA, complete cds.
 NT2NE20177210//Leishmania major partial ppg1 gene for proteophosphoglycan.
 NT2RP70012830//CALPHOTIN.
 NT2RP70035110//Caenorhabditis elegans UNC-89 (unc-89) gene, complete cds.
 15 NTONG20002230//Mus musculus RW1 protein mRNA, complete cds.
 NTONG20005310//Ribosomal protein S9/S16
 NTONG20029850//CALCYPHOSINE (R2D5 ANTIGEN).
 NTONG20035150//RING CANAL PROTEIN (KELCH PROTEIN).
 NTONG20058220//Homo sapiens phosphoprotein pp75 mRNA, partial cds.
 20 OCBBF20005220//Rattus norvegicus Fos-related antigen mRNA, complete cds.
 OCBBF20011860//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.
 OCBBF20016810//enhancer of polycomb [Mus musculus]
 OCBBF20147070//DNA polymerase (viral) C-terminal domain
 OCBBF20160380//liver stage antigen LSA-1 - Plasmodium falciparum OCBBF20177910//Corticotropin-releasing factor
 25 tor family
 PEBLM20005020//Virion host shutoff protein
 PLACE60055460//Homo sapiens leucine-zipper protein FKSG13 (FKSG13) mRNA, complete cds.
 PLACE60068710//SUPPRE PROTEIN SRP40.
 PLACE60080360//mucin [Homo sapiens]
 30 PLACE60082850//Pathogenesis-related protein Bet v I family
 PLACE60098350//Human hepatocellular carcinoma associated protein (JCL-1) mRNA, complete cds.
 PLACE60105680//Homo sapiens mRNA for TU12B1-TY, complete cds.
 PLACE60119700//Homo sapiens mRNA for ABP32, complete cds.
 PLACE60120280//SER/THR-RICH PROTEIN T10 IN DGCR REGION.
 35 PLACE60132200//TRICHOHYALIN.
 PLACE60181870//Pentaxin family
 PROST20084470//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds.
 PROST20087240//gag gene protein p24 (core nucleocapsid protein)
 PROST20122490//Gallus gallus syndesmos mRNA, complete cds.
 40 PROST20130320//S-100/ICaBP type calcium binding domain
 PROST20152870//Homo sapiens APC2 gene, exon 14.
 PUAEN10001640//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.
 PUAEN20000800//Bleomycin resistance protein
 SMINT20012220//Collagen triple helix repeat (20 copies)
 45 SMINT20035510//Drosophila melanogaster La related protein (Iarp) mRNA, partial cds.
 SMINT20036440//Drosophila melanogaster epsin-like protein mRNA, complete cds.
 SMINT20038660//Homo sapiens HNOEL-iso (HNOEL-iso) mRNA, complete cds.
 SMINT20043390//Ras association (RalGDS/AF-6) domain
 SMINT20048720//Cytochrome P450// Cytochrome P450
 50 SMINT20052130//Rattus norvegicus mRNA for gankyrin homologue, complete cds.
 SMINT20054050//ABC1 PROTEIN HOMOLOG PRECURSOR.
 SPLEN20024770//Rattus norvegicus (rsec6) mRNA, complete cds.
 SPLEN20040780//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
 SPLEN20041810//BC-2 protein [Homo sapiens]
 55 SPLEN20100040//258.1 KDA PROTEIN C210RF5 (KIAA0933).
 SPLEN20104150//Ribosomal protein L36
 SPLEN20116720//Homo sapiens misato mRNA, partial cds.
 SPLEN20176130//Homo sapiens mRNA for ALEX1, complete cds.

- SPLEN20181570//TRICHOHYALIN.
 TESTI20004310//TRICHOHYALIN.
 TESTI20016970//TPR Domain
 TESTI20030440//TRICHOHYALIN.
 5 TESTI20043180//mouse mRNA for megakaryocyte potentiating factor, complete cds.
 TESTI20043910//IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
 TESTI20044900//Strongylocentrotus purpuratus radial spokehead mRNA, complete cds.
 TESTI20646110//Extracellular link domain
 10 TESTI20047930//Homo sapiens NY-REN-2 antigen mRNA, complete cds.
 TESTI20049410//Proprotein convertase P-domain
 TESTI20053950//IQ calmodulin-binding motif
 TESTI20054700//Streptococcus pneumoniae strain g375 surface protein PspC (pspC) gene, pspC-8. 1 allele, complete cds.
 15 TESTI20055880//Serum amyloid A protein
 TESTI20056030//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.
 TESTI20061090//Keratin, high sulfur B2 protein
 TESTI20064370//TPR Domain// TPR Domain// TPR Domain// TPR Domain// Synaptobrevin
 TESTI20084250//OXYSTEROL-BINDING PROTEIN.
 20 TESTI20092170//ENV polyprotein (coat polyprotein)
 TESTI20116050//UBX domain
 TESTI20120500//Kelch motif// Kelch motif
 TESTI20126280//Mus musculus STAP mRNA for sperm tail associated protein, complete cds.
 TESTI20144390//TESTIS-SPECIFIC PROTEIN PBS13.
 25 TESTI20165990//Ribosomal protein L36
 TESTI20169500//HYPOTHETICAL 51.9 KDA PROTEIN C27F1.04C IN CHROMOSOME I.
 TESTI20170280//Flagellar L-ring protein
 TESTI20176450//thioredoxin interacting factor [Mus musculus].
 TESTI20179230//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
 30 TESTI20180600//Homo sapiens HOM-TES-85 tumor antigen mRNA, complete cds.
 TESTI20209050//HYPOTHETICAL 113.1 KDA PROTEIN IN PRE5-FET4 INTERGENIC REGION.
 TESTI20210570//RETINAL-BINDING PROTEIN (RALBP).
 TESTI20215310//Homo sapiens calcyclin binding protein mRNA, complete cds.
 TESTI20247440//Human BLu protein testis isoform (BLu) mRNA, complete cds.
 35 TESTI20249360//Homo sapiens DEME-6 mRNA, partial cds.
 TESTI20250220//TRICHOHYALIN.
 TESTI20251440//Rattus norvegicus (rsec6) mRNA, complete cds.
 TESTI20255460//Mus musculus mRNA for MIWI (piwi), complete cds.
 THYMU20009500//TPR Domain
 40 THYMU20010180//MOB1 PROTEIN (MPS1 BINDER 1).
 THYMU20013810//Human SEC7 homolog Tic (TIC) mRNA, complete cds.
 THYMU20018250//TPR Domain
 THYMU20026950//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.
 THYMU20028410//Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.
 45 THYMU20030460//Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA, complete cds.
 THYMU20031330//Homo sapiens putative nucleotide binding protein mRNA, complete cds.
 THYMU20052460//PHORBOLIN I (FRAGMENTS).
 THYMU20055450//Zona pellucida-like domain
 THYMU20083830//Homo sapiens angiostatin binding protein 1 mRNA, complete cds.
 50 THYMU20139160//Uncharacterized protein family UPF0031
 THYMU20151610//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.
 TRACH20093400//TRICHOHYALIN.
 TRACH20104510//Uncharacterized protein family UPF0005
 TRACH20122980//HYPOTHETICAL PROTEIN MJ0798.
 55 TRACH20139280//PX domain
 TRACH20164810//D-isomer specific 2-hydroxyacid dehydrogenases
 TRACH20165540//Human alpha-1 type I collagen gene surrounding osteogenesis imperfecta OI type II deletion.
 UTERU20051790//guanylate kinase-interacting protein 1 Maguin-1, membrane-associated - rat

UTERU20083020//Domain of unknown function DUF71
 UTERU20121140//Rhodanese-like domain
 UTERU20128560//26.4 KDA PROTEIN IN RUVC-ASPS INTERGENIC REGION.
 UTERU20132620//AXONEME-ASSOCIATED PROTEIN MST101(2).
 5 UTERU20134830//pellino (Drosophila) homolog 2 [Homo sapiens]
 UTERU20181270//Zinc knuckle

[0091] Further, the reason is that a polypeptide does not always belong solely to a single category of the above-described functional categories, and therefore, a polypeptide may belong to any of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

10 **[0092]** Since the polypeptide encoded by clones of the invention contains full-length amino acid sequence, it is possible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation by expressing the polypeptide as a recombinant polypeptide using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the polypeptide.

[0093] The biological activities of respective polypeptides can be analyzed by the methods as shown below.

15
 Secretory protein, transmembrane protein:

[0094]

20 "Ion Channels" (Ed., R. H. Ashley, 1995) of "The Practical Approach Series" (IRL PRESS),
 "Growth Factors" (Eds., I. McKay, I. Leigh, 1993),
 "Extracellular Matrix" (Eds., M. A. Haralson, J. R. Hassell, 1995);

Glycoprotein-related protein:

25
[0095]

"Glycobiology" (Eds., M. Fukuda, A. Kobata, 1993) of "The Practical Approach Series" (IRL PRESS),
 "Glycoprotein Analysis in Biomedicine" (Ed., Elizabeth F. Hounsell, 1993) of "Method in Molecular Biology" (Humana Press) series;

Signal transduction-related protein:

35
[0096]

"Signal Transduction" (Ed., G. Milligan, 1992) of "The Practical Approach Series" (IRL PRESS),
 "Protein Phosphorylation" (Ed., D. G. Hardie, 1993), or
 "Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series;

40
 Transcription-related protein:

[0097]

45 "Gene Transcription" (Eds., B. D. Hames, S. J. Higgins, 1993) of "The Practical Approach Series" (IRL PRESS),
 "Transcription Factors" (Ed., D. S. Latchman, 1993); Enzyme and/or metabolism-related protein:
 "Enzyme Assays" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "The Practical Approach Series" (IRL PRESS); Cell division and/or cell proliferation-related protein:
 "Cell Growth, Differentiation and Senescence" (Ed., GEORGE STUDZINSKI, 2000) of "The Practical Approach Series" (IRL PRESS);

Cytoskeleton-related protein:

55
[0098]

"Cytoskeleton: Signalling and Cell Regulation" (Eds., KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY, 2000) of "The Practical Approach Series" (IRL PRESS),
 "Cytoskeleton Methods and Protocols" (Ed., Gavin, Ray H., 2000) of "Method in Molecular Biology" (Humana

Press) series; Nuclear protein and/or RNA synthesis-related protein:

"Nuclear Receptors" (Ed., DIDIER PICARD, 1999) of "The Practical Approach Series" (IRL PRESS),

"RNA Processing" (Eds., STEPHEN J. HIGGINS and B. DAVID HAMES, 1994);

5 Protein synthesis and/or transport-related protein:

[0099]

"Membrane Transport" (Ed., STEPHEN A. BALDWIN, 2000) of "The Practical Approach Series" (IRL PRESS)

10 "Protein Synthesis Methods and Protocols" (Eds., Martin, Robin, 1998) of "Method in Molecular Biology" (Humana Press) series;

Cellular defense-related protein:

15 **[0100]**

"DNA Repair Protocols" (Henderson, Daryl S., 1999) of "Method in Molecular Biology" (Humana Press) series,

"Chaperonin Protocols" (Eds., Schneider, Christine, 2000); Development and/or differentiation-related protein:

20 "Developmental Biology Protocols" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "Method in Molecular Biology" (Humana Press) series;

DNA- and/or RNA-binding protein:

[0101]

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"DNA-Protein Interactions Principles and Protocols" (Eds., Kneale, G. Geoff, 1994) of "Method in Molecular Biology" (Humana Press) series,

"RNA-Protein Interaction Protocols" (Eds., Haynes, Susan R., 1999);

30 ATP- and/or GTP-binding protein:

[0102]

"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series.

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[0103] In the categorization, the clone predicted to belong to the category of secretory and/or membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it was a secretory or membrane protein, or a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane region was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

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[0104] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

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[0105] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.

[0106] The clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes a transcription-related protein.

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[0107] The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, UniGene, or nr, where the hit data corresponds to genes or polypeptides which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is the human gene and disease database described later.

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[0108] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0109] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0110] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubules, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0111] The clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0112] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0113] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0114] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0115] The clone predicted to belong to the category of DNA-and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0116] The clone predicted to belong to the category of ATP-and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0117] As to a protein involved in a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database OMIM, which is a database of human genes and diseases, to analyze the protein. Further, new information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database. The proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0118] Also, as for a secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are involved in many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also, association between proteins related to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-gaku Zoukan, Vol.17, No.3), and "Gene Medicine" (1999) Vol.3, No.2). When cancer is used as an example, as described in "Biology of Cancer" (S. Matsubara, 1992) of Life Science series (Shokabo), many proteins are involved in cancers, which include enzyme and/or metabolism-related proteins, cytoskeleton-related proteins, cell division and/or cell proliferation-related proteins as well as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins. As clearly seen by the above example, it is evident that not only disease-related proteins but also secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, etc. are often involved in diseases, and thus they can be useful targets in the field of medical industry.

[0119] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

- (1) secretion protein,
- (2) membrane protein,
- (3) channel, and
- (4) extracellular matrix were used.

[0120] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein

354 entries found, searching for "secretion protein"

*604667, *104760, *176860, *151675, *139320, *107400, *604029, *118910, #200100, *176880, *603850, *147572, *604028, *179513, *125950, *139250, *246700, *600946, *600560, *602926, 185860, *605083, *603215,

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2) Membrane protein

1489 entries found, searching for "membrane protein"

*130500, *605704, *305360, *153330, *173610, *109270, *170995, *170993, *104776, *602333, *309060, *605703, *120920, *605943, *602690, *159430, *600897, *133090, *601178, *602413, *602003, *604405, *605940, *603237, *109280, *600378, *602173, *107776, *602334, *602335, *125305, *601134, *309845, *605731, *154045, *603241, *603718, *600594, *603214, *185881, *603657, *600182, *603177, *605331, *601476, *605456, *601114, *605190, *600723, *603904, *136950, *300222, *602879, *185880, *605348, *300096, *602257, *177070, *310200, *603062, *603344, *600039, *602977, *300100, *128240, *600959, *600322, *227400, *186945, *600946, *602534, *602048, *182900, *601097, *600267, *602625, *136430, *602421, *601047, *107450, *143450, *603141, *184756, *164730, *159440, *154050, *600579, *312080, *604202, *603700, *600447, *256540, *604691, *158343, *600403, *602414, *137290, *176640, *176981, *600179, *600754, *604456, *604693, *605875, *604605, *188860, *300172, *602910, *604323, *219800, *601848, *603179, *600279, *602251, #222700, *603831, *605072, *605377, *601028, *604155, *108733, *104225, *601896, *601510, *173335, *107770, *601767, *600046, *603850, *600040, *603784, *603234, 188560, *605863, *121015, *605862, *605861, *186946, *604252, *603215, *142461, *604597, *603143, *605264, *603735, *176860, *605536, *176801, *180721, *603355, *104760, *131560, *310300, *602631, *304700, #309400, *603142, *143890, *605431, *600753, *115501, *176790, *600266, *601691, *168468, *601239, *602216, #104300, *605613, *601595, *605550, *125950, *605475, *602217, *602261, *603534, *602262, *604631, *190315, *601313, *604306, *104311, *604672, *605000, *602461, *605548, *602296, *604376, *121014, *121011, *600691, *604262, *139310, *304040, *605445, *179514, *179512, *151460, #160900, *120130, *128239, *601158, *601403, *176943, *601014, 300800, *300294, *601757, *185470, *273800, *605034, *602887, #185000, *604871, *603593, *603583, *605454, *104775, *605872, *141180, *602713, *603531, *139150,

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3) Channel (member of membrane protein)

361 entries found, searching for "channel"

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4) Extracellular matrix

218 entries found, searching for "extracellular matrix"

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[0121] In addition to these, the various keywords shown in the above-mentioned categorization or others can be used for the OMIM search and the result may suggest the involvement thereof in diseases.

[0122] Further, the use of nucleotide sequences of cDNAs of the present invention enables analyzing the expression frequency of genes corresponding to the cDNAs. In addition, functions of the genes can be predicted based on the information obtained by the expression frequency analysis.

[0123] There are several methods for analyzing the expression levels of genes involved in diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods using, for example, Northern hybridization, RT-PCR, DNA microarray, etc. (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Nawa (eds.), Shujunsha (2000)). By computer analysis, in addition to these analysis methods, the nucleotide sequences of expressed genes can be compared to analyze the expression frequency. For example, there is a database called "BODYMAP"; gene clones are extracted at random from cDNA libraries of various tissues and/or cells, and the clones homologous to one another are assigned to a single cluster based on the information of nucleotide sequence homology at the 3'-end; genes are classified into any clusters, and the numbers of clones in the respective clusters are compared to gain the information on expression frequency (<http://bodymap.ims.u-tokyo.ac.jp/>).

[0124] When explicit difference in the expression levels between diseased tissues and normal tissues is observed for a gene by these analytical methods, it can be concluded that the gene is closely involved in a disease or disorder. Instead of diseased tissues, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely involved in a disease or disorder.

[0125] From the 1970 clones whose full-length nucleotide sequences had been revealed, genes involved in particular pathology or functions were selected by the use of databases shown below (see Example 7; "Expression frequency analysis *in silico*"). The database used in the analyses of the present invention contains nucleotide sequences of 770,546 clones, and the population of the database is large enough for the analysis. The sequence information in the database was obtained by selecting cDNA clones at random from cDNA libraries derived from the various tissues and cells shown in Example 1 and determining the 5'-end sequences thereof.

[0126] Then, the nucleotide sequences of respective clones in this database were categorized (clustered) based on the nucleotide sequence homology determined with a search program; the number of clones belonging to every cluster of each library was determined and normalized; thus, the ratio of a certain gene in a cDNA library was determined. This analysis provided the information of the expression frequency of a gene in a tissue or cell that is the source of the cDNA library.

[0127] Then, in order to analyze the expression of genes corresponding to the nucleotide sequences of cDNAs of the present invention in tissues and cells, the libraries from the tissues or cells, which had been used in the large-scale cDNA analyses, were taken as subjects to compare the expression levels between different tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues or cells from which 600 or more cDNA clones whose nucleotide sequences had been analyzed were derived. The result of this analysis showed that the cDNA clones corresponded to the genes involved in the pathology and functions, which are indicated below. Each value in Tables 3 to 39 indicated below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0128] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of

bone. The onset correlates to the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are genes involved in osteoporosis relevant to bone metabolism.

- 5 **[0129]** A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were 26 clones indicated in Table 3. These clones are involved in osteoporosis.

Genes involved in neural cell differentiation

- 15 **[0130]** Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

- 20 **[0131]** A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were 193 clones indicated in Table 4. These genes are neurological disease-related genes.

25 Cancer-related genes

- [0132]** It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression thereof can contribute to the carcinogenesis in tissues and cells. Thus, genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

- 30 **[0133]** The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were 4 clones indicated in Table 5.

- 35 **[0134]** The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two was one clone indicated in Table 6.

- [0135]** The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two was one clone indicated in Table 7.

- 40 **[0136]** The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were 6 clones indicated in Table 8.

- [0137]** . The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were 132 clones indicated in Table 9.

- 45 **[0138]** The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were 25 clones indicated in Table 10.

- [0139]** The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were 99 clones indicated in Table 11.

- 50 **[0140]** The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were 3 clones indicated in Table 12.

- 55 **[0141]** The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were 15 clones indicated in Table 13.

- [0142]** The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were 97 clones indicated in

Table 14.

[0143] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were 203 clones indicated in Table 15.

[0144] These genes are involved in cancers.

[0145] Further, there is a method to search for genes involved in development and differentiation, which is the expression frequency analysis in which the expression levels of genes are compared between developing and/or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0146] By using the information of gene expression frequency gained from the database of 5'-end nucleotide sequences described above, genes involved in development or differentiation of particular tissues were selected from the 1970 clones whose full-length nucleotide sequence had been revealed (see Example 7).

[0147] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were 775 clones indicated in Tables 16 to 36.

[0148] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were 28 clones indicated in Table 37.

[0149] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were 95 clones indicated in Table 38.

[0150] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were 99 clones indicated in Table 39. These genes are involved in regeneration of tissues and/or Cells.

[0151] The expression frequency or the like can be analyzed by PCR based on the nucleotide sequences of cDNAs of the present invention. There are some known methods for comparing the quantities of amplification products obtained by PCR. For example, the band intensities can be determined by ethidium bromide staining. With RI-labeled or fluorescently labeled primers, the RI signal or fluorescence intensity can be assayed for the quantity of labeled amplification products. Alternatively, the quantity of amplification products can also be determined by measuring the RI signal or the fluorescence intensity from the RI-labeled or fluorescently labeled probe hybridizing to the products. The assay results thus obtained are compared and then the clones exhibiting differences in the expression levels can be selected.

[0152] There are some quantitative PCR methods: a PCR method using internal standards; a competitive PCR, in which the quantification is achieved by adding, to a sample, a dilution series of a known quantity of a template RNA and by comparing the quantity of an amplification product derived from the RNA of interest with the quantity of an amplification product derived from the template RNA. These methods overcome the problems of errors in the amount of amplification products among tubes and of the plateau effect. ATAC-PCR (Adaptor-tagged competitive PCR) is a method of competitive PCR which is practiced by using multiple adaptors of different sizes attached to a gene whose 3'-end nucleotide sequence has previously been determined. The ratio of expression frequency of a single mRNA species from a number of tissues (cells) can be assayed in a single step (Nucleic Acids Research 1997, 25(22): 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112).

[0153] If it is observed, by using these analytical methods, that the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-related genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes involved in diseases and/or disorders affecting the tissues.

[0154] For example, inflammation is an important biological response that is known to be involved in various diseases. The representative inflammation-inducing factors include TNF- α (Tumor Necrosis Factor-alpha). There exists a signaling cascade activated by TNF- α stimulations, wherein NF- κ B is a transducing molecule (Cell 1995, 80:529-532). It has also been revealed that many inflammation-related genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the pathway (Trends Genet. 1999, 15(6): 229-235). It is assumed that genes whose expression levels are varied in response to the stimulation of TNF- α also participate in inflammation.

[0155] Further, the infection of *Helicobacter pylori* to the gastric epithelia is known to cause gastritis and gastroduodenal ulcer (Mebio 2000, July, 17(7): 16-33). Thus, the genes whose expression levels are altered depending on co-culturing cells with *Helicobacter pylori* may be involved in gastritis and gastroduodenal ulcer. A recent study has suggested that *Helicobacter pylori* strongly activates the NF- κ B pathway (Gastroenterology 2000, 119: 97-108).

[0156] THP-1 cell, which is a human monocyte cell line, was cultured in the presence of TNF- α (Tumor Necrosis

Factor- α). The genes whose expression levels were altered owing to the presence of TNF- α were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of TNF- α were ASTRO20055530, ASTRO20055930, ASTRO20088950, BRAMY20027390, BRAMY20076130, BRAMY20118410, BRAMY20125360, BRAMY20237190, BRCAN20001480, BRHIP10000720, CD34C20001750, CTONG20078340, CTONG20085210, DFNES20063460, FCBBF20029280, FCBBF20033360, FCBBF30078600, FEBRA20007820, FEBRA20031280, FEBRA20031810, FEBRA20040290, HLUNG20041540, HLUNG20092530, MESAN20021860, MESAN20067430, MESAN20084150, NT2NE20092950, NT2RP70031070, OCBBF20012520, OCBBF20142290, OCBBF20165900, OCBBF20170350, OCBBF20176650, PLACE60006300, PROST20011160, PROST20106060, SPLEN20040780, SPLEN20110860, SPLEN20177400, TESTI20030610, TESTI20043130, TESTI20059370, TESTI20254480, THYMU10004280, THYMU20030460, THYMU20062520, THYMU20078240, THYMU20150190, TRACH20090060, TRACH20125620, UTERU20026620, UTERU20045200, UTERU20064120, UTERU20103200.

[0157] On the other hand, the clones whose expression levels were decreased owing to the presence of TNF- α were BNGH420052350, BRACE20052530, BRAMY20003880, CTONG20170940, FCBBF30022680, FCBBF30225930, FCBBF30257370, FEBRA20046280, KIDNE20084030, KIDNE20188630, NT2NE20082130, OCBBF20110210, PLACE60061370, PROST20041460, PROST20075280, PROST20110120, SMINT20006020, TESTI20046540, TESTI20057200, TESTI20113940, TESTI20257910, TESTI20262940, TRACH20149740.

[0158] These clones are inflammation-related genes.

[0159] MKN45, which is a gastric cancer cell line, was co-cultured with *Helicobacter pylori*. The genes whose expression levels were altered owing to the presence of *Helicobacter pylori* were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of *Helicobacter pylori* were BRAMY20028530, BRAMY20035380, OCBBF20170350, PROST20011160, SKMUS20091900, SPLEN20040780, THYMU20078240, TRACH20190460, UTERU20045200, UTERU20064120, ASTRO20055530, CTONG20170940, FEBRA20040290, MESAN20067430, PROST20016760, THYMU10004280, TRACH20090060, UTERU20041970, OCBBF20142290, TESTI20030610.

[0160] On the other hand, the clones whose expression levels were decreased owing to the presence of *Helicobacter pylori* were

ASTRO20088950, BRACE20052530, BRAMY20003880, BRAMY20027390, BRAMY20036530, BRAMY20118410, BRHIP20000210, FCBBF20032930, FCBBF30022680, FCBBF30169870, FEBRA20182030, KIDNE20182540, LIVER20007750, MESAN20021220, NT2NE20059210, NT2NE20082130, OCBBF20155030, PROST20065100, PROST20075280, SPLEN20110860, TESTI20057200, TESTI20113940, TESTI20149880, TESTI20151800, TESTI20198600, TESTI20257910, THYMU20046770, THYMU20058550, THYMU20150190, FCBBF20033360, FCBBF30257370, FEBRA20098040, SMINT20006020.

[0161] These clones are involved in gastritis or gastroduodenal ulcer.

[0162] For example, if the polypeptide encoded by the cDNA of the present invention is a regulatory factor of cellular conditions such as growth and differentiation, it can be used for developing medicines as follows. The polypeptide or antibody provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible -to screen low molecular weight compounds, etc. by measuring the change in the cellular conditions, or the activation or inhibition of a particular gene. The screening can be performed as follows.

[0163] First, the polypeptide is expressed and purified as recombinant. The purified polypeptide is microinjected into cells such as various cell lines, or primary culture cells, and the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose expression is known to be involved in a particular change of cellular conditions may be detected by the amount of mRNA or polypeptide. Alternatively, the amount of intracellular molecules (low molecular weight compounds, etc.) that is changed by the function of the gene product (polypeptide) which is known to be involved in a particular change of cellular conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable) can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions.

[0164] Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening. If the gene product is turn out to be involved in a particular change in the cellular conditions, the change of the product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit the function of the polypeptide of the invention, it can be applied for developing medicines.

[0165] If the polypeptide encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein involved in signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0166] In case of a membrane protein, it is most likely to be a polypeptide that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0167] For example, a ligand against the polypeptide of the invention can be screened in the following manner.

Namely, a ligand that binds to a specific polypeptide can be screened by a method comprising the steps of: (a) contacting a test sample with the polypeptide of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said polypeptide, said partial peptide, or said cells.

[0168] On the other hand, for example, screening using cells expressing the polypeptide of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific polypeptide by using procedures (a) attaching the sample cells to the polypeptide of the invention or its partial peptide, and (b) selecting cells that can bind to the said polypeptide or its partial peptide.

[0169] In a following screening as an example, first the polypeptide of the invention is expressed, and the recombinant polypeptide is purified. Next, the purified polypeptide is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjiyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A polypeptide of the invention can be labeled with RI such as 125 I, and enzyme (alkaline phosphatase etc.).

[0170] Alternatively, a polypeptide of the invention may be used without labeling and then detected by using a labeled antibody against the polypeptide. The cells that are selected by the above screening methods, which express a receptor of the polypeptide of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0171] Once the ligand binding to the polypeptide of the invention, the receptor of the polypeptide of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0172] When the polypeptide of the invention is a receptor, the screening method comprises the steps of (a) contacting the polypeptide of the invention or cells expressing the polypeptide of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said polypeptide or cells expressing said polypeptide and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the polypeptide of the invention is a ligand, the screening method comprises the steps of (a) contacting the polypeptide of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the polypeptide and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0173] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the polypeptide of the invention can also be used as a sample.

[0174] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the polypeptide. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the polypeptide and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the polypeptide and its associated proteins (including a receptor) *in vivo*. Such compounds can be used for developing drugs for precaution or cures of a disease in which the polypeptide is involved.

[0175] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0176] The screening can be performed, for example, as follows. First, the polypeptide of the invention is expressed and purified in a recombinant form. Then, the purified polypeptide is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and polypeptide. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (polypeptide) that is known to function in a certain cellular change is used for the detection.

[0177] Once the screening reveals that then polypeptide of the invention can regulate cellular conditions or the functions, it is possible to apply the polypeptide as a pharmaceutical and diagnostic medicine for related diseases by itself or by altering a part of it into an appropriate composition.

[0178] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the polypeptide of the invention

and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the polypeptide may play a certain role.

[0179] Proteins involved in signal transduction or transcription may be a factor that affects a certain polypeptide or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a polypeptide or gene by expressing the polypeptide provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular polypeptide or gene.

[0180] The screening may be performed as follows. First, a transformed cell line expressing the polypeptide is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or polypeptide. Alternatively, the amount of an intracellular molecule (low molecular weight compounds, etc.) that is changed by the function of a certain gene product (polypeptide) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, β -galactosidase, etc.) into a cell, expressing the polypeptide provided by the invention into the cell, and estimating the activity of a marker gene product (polypeptide).

[0181] If the polypeptide or gene of the invention is involved in diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the polypeptide of the present invention.

[0182] For example, the polypeptide of the invention is expressed and purified as a recombinant polypeptide. Then, the polypeptide or gene that interacts with the polypeptide of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the polypeptide of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0183] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases in which the polypeptide of the present invention is involved. Similarly, if the regulatory factor obtained in the screening is turn out to be a polypeptide, compounds that can newly affect the expression or activity of the polypeptide may be used as a medicine for the diseases in which the polypeptide of the invention is involved.

[0184] If the polypeptide of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins involved in signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the polypeptide of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the polypeptide.

[0185] In a screening given as an example, the polypeptide of the invention is expressed and the recombinant polypeptide is purified. Then, compounds are contacted with the purified polypeptide, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified polypeptide is added, and the amount of the substrate and the reaction products is examined.

[0186] The compounds obtained in the screening may be used as a medicine for diseases in which the polypeptide of the invention is involved. Also they can be applied for tests that examine whether the polypeptide of the invention functions normally *in vivo*.

[0187] Whether the secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein of the present invention is a novel protein involved in diseases or not is determined in another method than described above, by obtaining a specific antibody against the polypeptide of the invention, and examining the relationship between the expression or activity of the polypeptide and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0188] Proteins involved in diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the related disease or a target of gene therapy.

[0189] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by polynucleotide, the polynucleotide can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the polynucleotide and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0190] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or polypeptide, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 1. The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0191] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0192] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known polypeptides. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0193] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the polypeptide encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0194] The present invention has provided 1970 polynucleotides. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. It is known that secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, and so on are involved in many diseases. The genes and proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0195] In particular, cDNA assumed to encode secretory proteins, which were provided by this invention, are very important for the industry since the encoded proteins themselves are expected to be useful as pharmaceutical agents and many disease-related genes may be included in them. In addition, membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, and genes encoding them can be used as indicators for diseases, etc. These cDNA are also very important for the industry, which are expected to regulate the activity or expression of the encoded protein to treat diseases, etc.

[0196] Any patents, patent applications, and publications cited herein are incorporated by reference.

[0197] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Preparation of cDNA library by oligo-capping

(1) Extraction and purchase of mRNA

[0198] Total RNAs as mRNA sources were extracted from human tissues (shown below) by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989). Further, by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989), total RNAs as mRNA sources were extracted from human culture cells and human primary culture cells (shown below) which had been cultivated by the methods described in the catalogs.

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[0199] The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Extraction of mRNA from human tissues>

[0200]

NTONG: Normal tongue;
CTONG: Tongue cancer;
FCBBF: Fetal brain;
OCBBF: Fetal brain;
PLACE: Placenta;
SYNOV: Synovial membrane tissue (from rheumatoid arthritis).

<Extraction of mRNA from culture cells>

[0201]

BNGH4: H4 cells (ATCC #HTB-148);
IMR32: IMR32 cells (ATCC #CCL-127);
SKNMC: SK-N-MC cells (ATCC #HTB-10);
3NB69: NB69 cells (RCB #RCB0480);
BGGI1: GI1 cells (RCB #RCB0763);
NB9N4: NB9 cells (RCB #RCB0477);
SKNSH: SK-N-SH cells (RCB #RCB0426);
NT2RM: NT2 cells (STARATAGENE #204101);
NT2RP: NT2 cells treated with retinoic acid (RA) for 5 weeks to induce the differentiation;
NT2RI: NT2 cells treated with RA for 5 weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks;
NT2NE: NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant neurons were concentrated and harvested (NT2 Neuron);
NTISM: NT2 cells (STARATAGENE #204101) were treated with RA for 5 weeks to induce the differentiation, and then treated with the growth inhibitor for 2 weeks; mRNA was prepared from the cells and a cDNA library was constructed from the mRNA; the cDNAs of the library whose nucleotide sequences were shared by those of mRNAs from undifferentiated NT2 cells were subtracted by using a Subtract Kit (Invitrogen #K4320-01); the subtracted library (NT2RI-NT2RM) was provided by this procedure.

[0202] RCB indicates that the cell was provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research; ATCC indicates that the cell was provided by American Type Culture Collection.

<Extraction of mRNA from primary culture cells>

[0203]

ASTRO: Normal human astrocyte NHA5732, Takara Shuzo #CC2565;
DFNES: Normal human dermal fibroblast (neonatal skin); NHDF-Neo NHDF2564, Takara Shuzo #CC2509;
MESAN: Normal human mesangial cell NHMC56046-2, Takara Shuzo #CC2559;
NHNPC: Normal human neural progenitor cell NHNP5958, Takara Shuzo #CC2599;
PEBLM: Normal human peripheral blood mononuclear cell HPBMC5939, Takara Shuzo #CC2702;
HSYRA: Human synoviocyte HS-RA (from rheumatoid arthritis), Toyobo #T404K-05;
PUAEN: Normal human pulmonary artery endothelial cells, Toyobo #T302K-05;
UMVEN: Normal human umbilical vein endothelial cell HUVEC, Toyobo #T200K-05;
HCASM: Normal human coronary artery smooth muscle cell HCASM, Toyobo #T305K-05;
HCHON: Normal human chondrocyte HC, Toyobo #T402K-05;
HHDP: Normal human dermal papilla cell HDPC, Toyobo #THPCK-001; CD34C: CD34+ cells (AllCells, LLC #CB14435M);
D3OST: CD34+ cells treated with the osteoclast differentiation factor (ODF) for 3 days to induce the differentiation;
D6OST: CD34+ cells treated with ODF for 6 days to induce the differentiation;

D9OST: CD34+ cells treated with ODF for 9 days to induce the differentiation.

[0204] Then, total RNAs extracted from the following human tissues were purchased and used as mRNA sources. The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Purchase of total RNA containing mRNA extracted from human tissues>

[0205]

ADRGL: Adrenal gland, CLONTECH #64016-1;
 BRACE: Brain (cerebellum), CLONTECH #64035-1;
 BRAWH: Whole brain, CLONTECH #64020-1;
 FEBRA: Fetal brain, CLONTECH #64019-1;
 FELIV: Fetal liver, CLONTECH #64018-1;
 HEART: Heart, CLONTECH #64025-1;
 HLUNG: Lung, CLONTECH #64023-1;
 KIDNE: Kidney, CLONTECH #64030-1;
 LIVER: Liver, CLONTECH #64022-1;
 MAMGL: Mammary Gland, CLONTECH #64037-1;
 PANCR: Pancreas, CLONTECH #64031-1;
 PROST: Prostate, CLONTECH #64038-1;
 SALGL: Salivary Gland, CLONTECH #64026-1;
 SKMUS: Skeletal Muscle, CLONTECH #64033-1;
 SMINT: Small Intestine, CLONTECH #64039-1;
 SPLEN: Spleen, CLONTECH #64034-1;
 STOMA: Stomach, CLONTECH #64090-1;
 TBAES: Breast (Tumor), CLONTECH #64015-1;
 TCERX: Cervix (Tumor), CLONTECH #64010-1;
 TCOLN: Colon (Tumor), CLONTECH #64014-1;
 TESTI: Testis, CLONTECH #64027-1;
 THYMU: Thymus, CLONTECH #64028-1;
 TLUNG: Lung (Tumor), CLONTECH #64013-1;
 TOVAR: Ovary (Tumor), CLONTECH #64011-1;
 TRACH: Trachea, CLONTECH #64091-1;
 TUTER: Uterus (Tumor), CLONTECH #64008-1;
 UTERU: Uterus, CLONTECH #64029-1;
 ADIPS: Adipose, Invitrogen #D6005-01;
 BLADE: Bladder, Invitrogen #D6020-01;
 BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01;
 CERVX: Cervix, Invitrogen #D6047-01;
 COLON: Colon, Invitrogen #D6050-0;
 NESOP: Esophagus, Invitrogen #D6060-01;
 PERIC: Pericardium, Invitrogen #D6105-01;
 RECTM: Rectum, Invitrogen #D6110-01;
 TESOP: Esophageal (Tumor), Invitrogen #D6860-01;
 TKIDN: Kidney (Tumor), Invitrogen #D6870-01;
 TLIVE: Liver (Tumor), Invitrogen #D6880-01;
 TSTOM: Stomach (Tumor), Invitrogen #D6920-01;
 BEAST: Adult breast, STARATAGENE #735044;
 FEHRT: Fetal heart, STARATAGENE #738012;
 FEKID: Fetal kidney, STARATAGENE #738014;
 FELNG: Fetal lung, STARATAGENE #738020;
 NOVAR: Adult ovary, STARATAGENE #735260;
 BRASW: subtracted library (BRALZ-BRAWH). A cDNA library was constructed from mRNA prepared from tissues of cerebral cortex obtained from an Alzheimer patient [BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01]; the cDNAs of this library whose nucleotide sequences were shared by those of mRNAs from whole brain tissue [BRAWN: Whole brain, CLONTECH #64020-1] were subtracted by using

a Subtract Kit (Invitrogen #K4320-01).

[0206] Further, mRNAs extracted and purified as poly A(+) RNAs from the human tissues shown below were purchased. A cDNA library was prepared from an RNA mixture in which the poly A(+) RNA from each tissue had been combined with poly A(-) RNA. The poly A(-) RNA was prepared by removing poly A(+) RNA from the total RNA of whole brain tissue (CLONTECH #64020-1) by using oligo dT cellulose. The library names and the origins are indicated below in the order of "Library name: Origin".

<Purchase of mRNAs of human tissues as poly A(+) RNAs>

[0207]

BRAMY: Brain (amygdala), CLONTECH #6574-1;
BRCAN: Brain (caudate nucleus), CLONTECH #6575-1;
BRCOC: Brain (corpus callosum), CLONTECH #6577-1;
BRHIP: Brain (hippocampus), CLONTECH #6578-1;
BRSSN: Brain (substantia nigra), CLONTECH #6580-1;
BRSTN: Brain (subthalamic nucleus), CLONTECH #6581-1;
BRTHA: Brain (thalamus), CLONTECH #6582-1.

(2) Preparation of cDNA library

[0208] cDNA library was prepared from each RNA by the improved method (WO 01/04286) of oligo capping [M. Maruyama and S. Sugano, Gene, 138: 171-174 (1994)]. A series of procedures, BAP (Bacterial Alkaline Phosphatase) treatment, TAP (Tobacco Acid Pyrophosphatase) treatment, RNA ligation, first strand cDNA synthesis and RNA removal, were carried out using the oligo-cap linker (SEQ ID NO: 4093) and oligo dT primer (SEQ ID NO: 4094), as described in WO 01/04286. Then, the single-stranded cDNA was converted to a double-stranded cDNA by PCR (polymerase chain reaction) using 5' (SEQ ID NO: 4095) and 3' (SEQ ID NO: 4096) PCR primers, and then digested with *Sfi*. Then, a fraction of cDNA fragments, typically 2-kb or longer (3-kb or longer in some cases), was unidirectionally cloned into a *Dra*III-digested pME18SFL3 vector (Figure 1) (GenBank AB009864, Expression vector); the cDNA library was thus prepared.

[0209] The names of cDNA libraries, which were used in the analysis of full-length cDNA sequences, and their origins are shown in Table 2.

Table 2

Library	Type	Origin etc.
ADRGL	Tissue	Adrenal gland (CLONTECH #64016-1)
ASTRO	Primary culture cell	Normal Human Astrocyte NHA5732 (Takara Shuzo #CC2565)
BGGI1	Culture cell	GI1 cells (RCB #RCB0763)
BNGH4	Culture cell	H4 cells (ATCC #HTB-148)
BRACE	Tissue	Brain, cerebellum (CLONTECH #64035-1)
BRAMY	Tissue	Brain, amygdala (CLONTECH #6574-1)
BRAWH	Tissue	Brain, whole (CLONTECH #64020-1)
BRCAN	Tissue	Brain, caudate nucleus (CLONTECH #6575-1)
BRCOC	Tissue	Brain, corpus callosum (CLONTECH #6577-1)
BRHIP	Tissue	Brain, hippocampus (CLONTECH #6578-1)
BRSSN	Tissue	Brain, substantia nigra (CLONTECH #6580-1)
CD34C	Primary culture cell	CD34+ cells (AllCells, LLC #CB14435M)
CTONG	Tissue	Tongue, Cancer
DFNES	Primary culture cell	Normal Human Dermal Fibroblasts (Neonatal Skin); NHDF-Neo NHDF2564 (Takara Shuzo #CC2509)

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Table 2 (continued)

Library	Type	Origin etc.
FCBBF	Tissue	Brain, Fetal
FEBRA	Tissue	Brain, Fetal (CLONTECH #64019-1)
HCHON	Primary culture cell Tissue	Human Chondrocytes HC (Toyobo #T402K-05)
HEART		Heart (CLONTECH #64025-1)
HHDPC	Primary culture cell	Human dermal papilla cells HDPC (Toyobo #THPCK-001)
HLUNG	Tissue	Lung (CLONTECH #64023-1)
KIDNE	Tissue	Kidney (CLONTECH #64030-1)
LIVER	Tissue	Liver (CLONTECH #64022-1)
MESAN	Primary culture cell	Normal human mesangial cells NHMC56046-2 (Takara Shuzo #CC2559)
NESOP	Tissue	Esophagus (Invitrogen #D6060-01)
NT2NE	Culture cell	NT2 cells concentrated after differentiation (NT2 Neuron)
NT2RI	Culture cell	NT2 cells treated by growth inhibitor for 2 weeks after RA induction for 5 weeks
NT2RP	Culture cell	NT2 cells treated by RA for 5 weeks
NTONG	Tissue	Tongue
OCBBF	Tissue	Brain, Fetal
PANCR	Tissue	Pancreas (CLONTECH #64031-1)
PEBLM	Primary culture cell	Human peripheral blood mononuclear cells HPBMC5939 (Takara Shuzo #CC2702)
PLACE	Tissue	Placenta
PROST	Tissue	Prostate (CLONTECH #64038-1)
PUAEN	Primary culture cell	Human pulmonary artery endothelial cells (Toyobo #T302K-05)
SALGL	Tissue	Salivary Gland (CLONTECH #64026-1)
SKMUS	Tissue	Skeletal Muscle (CLONTECH #64033-1)
SKNMC	Culture cell	SK-N-MC cells (ATCC #HTB-10)
SKNSH	Culture cell	SK-N-SH cells (RCB #RCB0426)
SMINT	Tissue	Small Intestine (CLONTECH #64039-1)
SPLEN	Tissue	Spleen (CLONTECH #64034-1)
TESOP	Tissue	Esophageal, Tumor (Invitrogen #D6860-01)
TESTI	Tissue	Testis (CLONTECH #64027-1)
THYMU	Tissue	Thymus (CLONTECH #64028-1)
TKIDN	Tissue	Kidney, Tumor (Invitrogen #D6870-01)
TRACH	Tissue	Trachea (CLONTECH #64091-1)
UMVEN	primary culture cell	Human umbilical vein endothelial cells HUVEC (Toyobo #T200K-05)
UTERU	Tissue	Uterus (CLONTECH #64029-1)

[0210] The cDNA library with the high fullness ratio (the fullness ratio of 5'-end, which was calculated for each cDNA library by using the protein coding region found in known mRNA species as an index, was 90% in average) prepared by the improved oligo-capping method was constructed by using a eukaryotic expression vector pME18SFL3. The vector contains SR α promoter and SV40 small t intron in the upstream of the cloning site, and SV40 polyA added signal

sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical 'DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SR α promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells, etc. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

(3) Assessment of the 5'-end completeness of clones derived from the cDNA library prepared by oligo-capping

[0211] With respect to the plasmid DNAs of clones derived from the libraries, the nucleotide sequences of cDNA 5'-ends (3'-ends as well in some cases) were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed based on the obtained data.

[0212] The 5'-end completeness of about 770,000 clones derived from the human cDNA libraries prepared by the improved oligo-capping method was determined by the following method. The clones whose 5'-end sequences were consistent with those of known human mRNA in the public database were judged to be "full-length" if they had a longer 5'-end sequence than that of the known human mRNA; or even though the 5'-end sequence was shorter, if it contained the translation initiation codon it was judged to have the "full-length" sequence. Clones which did not contain the translation initiation codon were judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones was determined by comparing with known human mRNA. As a result, the fullness ratio of the 5'-ends was 90%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high in the human cDNA clones obtained by the oligo-capping method.

EXAMPLE 2

Sequencing analysis of cDNA ends and selection of full-length clones

[0213] With respect to the plasmid DNAs of clones obtained from each cDNA library, the 5'-end nucleotide sequences of the cDNAs were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed using the data obtained.

[0214] For the analyzed 5'-end sequences of cDNA clones, the data with the annotation of "complete cds" in the GenBank and UniGene were searched by BLAST homology search. When identical to certain human mRNA sequences, such cDNA clones were excluded. Then, clustering was carried out. When the identity was 90% or higher, and the length of consensus sequence was 50 base pairs or longer, the cDNA clones were assumed to belong to an identical cluster, and thus clustered. cDNA clones longer in the 5' direction were selected from the members belonging to a cluster; if required, the 3'-end sequences of the selected clones were determined by the same analysis method as used to determine the 5'-end sequences. The data of the end sequences obtained were analyzed, and then the clones forming a sequence contig at 5'- and 3'-ends were excluded. Further, as mentioned above, the data was analyzed again by BLAST homology search; when identical to certain human mRNA sequences (including sequences patented and applied for), the cDNA clones were excluded. Thus, the cDNAs clones to be analyzed for their nucleotide sequence were obtained.

EXAMPLE 3

Analysis of the full-length nucleotide sequences

[0215] The full-length nucleotide sequences of the selected clones were determined. The nucleotide sequence determination was mainly performed by primer walking method comprising the dideoxy terminator method using custom-made synthetic DNA primers. Namely, the nucleotide sequences of the DNAs were determined in a sequencer from PE Biosystems, after sequencing reaction was carried out with a DNA sequencing reagent from the same supplier using the custom-made synthetic DNA primers according to the manual. A part of the clones were analyzed with a DNA sequencer from Licor.

[0216] Further, the nucleotide sequences of a part of the clones were determined by the shotgun method where the plasmids containing the cDNAs were digested at random were used, instead of the use of custom-made primers, by the same method in the DNA sequencer. The full-length nucleotide sequences were finally determined by completely assembling the partial nucleotide sequences obtained by the above method.

[0217] Then, the regions translatable to proteins were deduced from the determined full-length nucleotide sequences, and thereby the amino acid sequences were determined. SEQ ID NOs corresponding to the respective sequences are shown in Table 1.

EXAMPLE 4

Functional prediction by homology search

[0218] For the determined nucleotide sequences, GenBank, SwissProt, UniGene, and nr were searched by BLAST. The clones exhibiting higher homology, which were convenient to predict their functions based on the nucleotide sequences and deduced amino acid sequences, were selected based on the BLAST search hit data whose P value or E value was 10^{-4} or lower and for which the length of consensus sequence \times homology = 30 or higher in the amino acid database search. Further, from them, representative clones were selected, which are shown as Homology Search Result Data in the last part herein. Accordingly, the data shown herein are merely the representative data, and the molecule exhibiting homology to each clone is not limited thereto. Further, with respect to a part of clones, the BLAST search hit data that did not meet the criteria as described above are not shown herein.

EXAMPLE 5

Search for signal sequence, transmembrane domain and other functional domains in the deduced amino acid sequences

[0219] With respect to the amino acid sequences deduced from the full-length nucleotide sequences, the prediction was made for the presence of signal sequence at the amino terminus, the presence of transmembrane domain, and the presence of functional protein domains (motifs). The signal sequence at the amino terminus was searched for by PSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]; the transmembrane domain, by SOSUI [T. Hirokawa et al., Bioinformatics, 14: 378-379 (1998)] (Mitsui Knowledge Industry); the function domain, by Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>). The amino acid sequence in which the signal sequence at the amino terminus or transmembrane domain had been predicted to be present by PSORT or SOSUI were assumed to be a secretory or membrane protein. Further, when the amino acid sequence hit a certain functional domain by the Pfam functional domain search, the protein function can be predicted based on the hit data, for example, by referring to the function categories on the PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). In addition, the functional domain search can also be carried out on the PROSITE.

[0220] The search results obtained with the respective programs are shown below.

[0221] The clones whose deduced amino acid sequences were detected to have the signal sequences by PSORT are as follows.

ADRGL20021910, ADRGL20036380, ADRGL20063770, ASTRO20020240, BNGH420052350, BNGH420077980, BRACE20054080, BRACE20194670, BRAMY20044920, BRAMY20047560, BRAMY20137360, BRAMY20204270, BRAMY20237190, BRAMY20251750, BRAWH20020470, BRAWH20093070, BRCAN10001680, BRHIP10000720, BRSSN20091190, CD34C20001750, CTONG20059130, CTONG20069320, FCBBF30062490, FCBBF30132660, FEBRA20039260, FEBRA20040230, FEBRA20040560, FEBRA20046280, FEBRA20182030, HCHON10001660, HCHON20015050, HEART10001490, HHDPC20088160, HLUNG20032460, HLUNG20034970, HLUNG20050760, HLUNG20081390, HLUNG20088750, KIDNE20134130, KIDNE20143200, LIVER20007750, LIVER20010510, MESAN20021220, MESAN20027900, MESAN20095220, NT2NE20069580, NT2NE20082130, NT2NE20167660, NT2RP70003110, OCBBF20000740, OCBBF20012520, OCBBF20110730, OCBBF20118720, OCBBF20155030, OCBBF20170350, OCBBF20191950, PANC10000860, PEBLM20001800, PLACE60004260, PLACE60006300, PLACE60055590, PLACE60056910, PLACE60057860, PLACE60104630, PLACE60184870, PROST20050390, PROST20084680, PROST20105450, PROST20106060, PROST20110120, SKMUS20091900, SKNMC20006350, SMINT20024140, SMINT20028840, SMINT20086250, SMINT20088440, SMINT20088690, SPLEN20017810, SPLEN20073880, SPLEN20080070, SPLEN20101950, SPLEN20108000, SPLEN20110860, SPLEN20118050, SPLEN20138600, SPLEN20139100, SPLEN20193230, SPLEN20193490, SPLEN20201830, TESTI20043130, TESTI20047370, TESTI20057200, TESTI20059080, TESTI20061200, TESTI20063330, TESTI20063600, TESTI20102390, TESTI20116120, TESTI20151800, TESTI20166670, TESTI20210030, TESTI20245860, THYMU20020800, THYMU20046770, THYMU20050010, THYMU20054800, THYMU20055740, THYMU20083390, THYMU20115380, TRACH20081270, TRACH20159390, UTERU20040150, UTERU20064120, UTERU20086530, UTERU20127150

[0222] The clones whose deduced amino acid sequences were detected to have the transmembrane domains by SOSUI are as follows. Numerals indicate the numbers of transmembrane domains detected in the deduced amino acid

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sequences. Of the search result, the clone name and the number of transmembrane domains are demarcated by a double slash mark (/).

5 ADRGL20020290//10, ADRGL20021910//2, ADRGL20063770//2, ASTRO20010010//4, ASTRO20045840//3, ASTRO20053430//1, ASTRO20055530//1, ASTRO20055570//2, ASTRO20055930//2, ASTRO20075150//1, ASTRO20088950//1, ASTRO20091180//4, BNGH420021680//1, BNGH420023870//1, BNGH420052350//1, BNGH420059680//1, BNGH420075940//1, BNGH420087430//3, BRACE10000510//2, BRACE20052530//1, BRACE20066360//3, BRACE20068710//1, BRACE20069000//5, BRACE20069110//1, BRAMY10001730//1, BRAMY20001510//1, BRAMY20003880//1, BRAMY20024790//2, BRAMY20027390//2, BRAMY20028530//2, BRAMY20035380//2, BRAMY20045210//1, BRAMY20050940//3, BRAMY20053910//2, BRAMY20055760//5, 10 BRAMY20072440//8, BRAMY20083820//2, BRAMY20089770//1, BRAMY20096930//1, BRAMY20118410//1, BRAMY20123400//2, BRAMY20125550//1, BRAMY20127310//1, BRAMY20127760//1, BRAMY20135720//3, BRAMY20139440//5, BRAMY20152510//1, BRAMY20194680//2, BRAMY20204270//1, BRAMY20225320//2, BRAMY20237190//1, BRAMY20251750//1, BRAMY20285650//2, BRAWH20020470//7, BRAWH20026010//1, BRAWH20030000//2, BRAWH20039640//2, BRAWH20055330//1, BRAWH20078620//2, BRAWH20093040//3, 15 BRAWH20185270//5, BRAWH20190550//1, BRCAN10000760//10, BRCAN20001480//3, BRCAN20004180//1, BRCOC20000470//2, BRCOC20003600//1, BRHIP10001040//5, BRHIP20000210//1, BRSSN20001970//4, BRSSN20074640//2, CD34C20001750//1, CTONG20017490//1, CTONG20029030//4, CTONG20041260//9, CTONG20044870//2, CTONG20045500//2, CTONG20049480//3, CTONG20051450//1, CTONG20056150//2, CTONG20059130//6, CTONG20060040//1, CTONG20065680//1, CTONG20071680//13, CTONG20076810//1, 20 CTONG20078340//2, CTONG20079590//1, CTONG20083980//1, CTONG20084020//2, CTONG20167750//1, CTONG20168240//3, CTONG20179890//5, CTONG20183830//1, DFNES20018000//2, DFNES20028170//1, DFNES20029660//8, DFNES20072990//9, DFNES20080880//1, FCBBF20018680//3, FCBBF20029280//2, FCBBF20032930//1, FCBBF20036360//2, FCBBF20054390//2, FCBBF30022680//1, FCBBF30042610//7, FCBBF30062490//2, FCBBF30075970//1, FCBBF30078600//3, FCBBF30095410//1, FCBBF30105440//3, 25 FCBBF30118670//1, FCBBF30145670//1, FCBBF30164510//1, FCBBF30169870//1, FCBBF30172330//1, FCBBF30177290//2, FCBBF30179740//1, FCBBF30195690//2, FCBBF30197840//1, FCBBF30212210//1, FCBBF30223110//1, FCBBF30225930//9, FCBBF30230610//1, FCBBF30260480//5, FCBBF30266510//3, FCBBF30287940//1, FCBBF50000610//2, FCBBF50004950//3, FEBRA20007820//4, FEBRA20018670//2, FEBRA20031280//7, FEBRA20031810//2, FEBRA20040560//4, FEBRA20057010//1, FEBRA20080860//1, 30 FEBRA20084750//1, FEBRA20115930//10, FEBRA20116650//4, FEBRA20121950//5, FEBRA20141980//1, FEBRA20177800//1, FEBRA20182030//1, HCHON20015050//1, HEART20031680//1, HHDP10001140//1, HHDP20051850//1, HHDP20082790//3, HHDP20088160//1, HLUNG20015070//2, HLUNG20020850//2, HLUNG20029490//1, HLUNG20032460//1, HLUNG20033350//2, HLUNG20037160//2, HLUNG20050760//1, HLUNG20052300//1, HLUNG20060670//1, HLUNG20065990//1, HLUNG20074330//1, HLUNG20081390//2, 35 HLUNG20092530//1, KIDNE20016360//5, KIDNE20083150//3, KIDNE20084030//12, KIDNE20084800//2, KIDNE20086490//1, KIDNE20086660//2, KIDNE20094670//1, KIDNE20142900//1, KIDNE20148080//1, KIDNE20160960//2, KIDNE20163710//1, KIDNE20169180//2, KIDNE20182540//3, KIDNE20186170//1, KIDNE20188630//1, KIDNE20189960//1, LIVER20007750//8, LIVER20010990//4, LIVER20030650//6, LIVER20038000//4, MESAN20007110//1, MESAN20008150//3, MESAN20021220//2, MESAN20060430//1, 40 MESAN20067430//3, MESAN20084150//3, NT2NE20018740//1, NT2NE20039210//1, NT2NE20053230//1, NT2NE20059210//1, NT2NE20080770//1, NT2NE20082130//3, NT2NE20092950//1, NT2NE20152620//1, NT2NE20167660//1, NT2NE20181800//1, NT2RI20016240//2, NT2RI20021200//3, NT2RI20033920//5, NT2RP70027790//2, NT2RP70031070//10, NT2RP70031480//6, NT2RP70087140//1, OCBBF20000740//2, OCBBF20012520//2, OCBBF20109780//1, OCBBF20110210//2, OCBBF20110730//2, OCBBF20112280//3, 45 OCBBF20118720//3, OCBBF20123200//2, OCBBF20165910//9, OCBBF20176650//1, OCBBF20185630//1, OCBBF20191950//3, PANCR10000860//1, PLACE60004260//1, PLACE60006300//2, PLACE60053280//3, PLACE60056910//1, PLACE60057860//3, PLACE60061370//1, PLACE60070500//2, PLACE60104630//3, PLACE60107010//2, PLACE60184870//1, PROST20011160//2, PROST20014150//2, PROST20035830//1, PROST20050390//1, PROST20065100//7, PROST20073280//1, PROST20082430//1, PROST20084680//3, 50 PROST20105450//6, PROST20110120//1, PROST20114100//2, PROST20152510//4, PROST20168600//6, PUAEN10000870//2, SKMUS20006790//1, SKMUS20020770//1, SKNMC20006350//1, SKNSH20094350//2, SMINT20008110//3, SMINT20024140//1, SMINT20026200//1, SMINT20028840//1, SMINT20045470//1, SMINT20081330//2, SMINT20092160//1, SPLEN20015100//2, SPLEN20017610//1, SPLEN20017810//2, SPLEN20024620//2, SPLEN20054500//1, SPLEN20058180//1, SPLEN20085910//2, SPLEN20090880//2, 55 SPLEN20101950//5, SPLEN20104690//1, SPLEN20105100//2, SPLEN20110180//1, SPLEN20121790//1, SPLEN20125230//1, SPLEN20136700//1, SPLEN20175920//1, SPLEN20177400//2, SPLEN20182850//1, SPLEN20183950//1, SPLEN20190080//1, SPLEN20190770//1, SPLEN20193230//1, SPLEN20193790//1, SPLEN20204670//1, TESOP10000350//1, TESTI20006160//5, TESTI20038240//1, TESTI20043220//1,

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TESTI20046540//1, TESTI20046870//1, TESTI20050400//1, TESTI20051730//7, TESTI20053260//2,
 TESTI20053780//1, TESTI20057200//1, TESTI20057590//1, TESTI20061200//10, TESTI20062120//1,
 TESTI20063330//1, TESTI20063410//1, TESTI20068530//2, TESTI20070400//10, TESTI20070740//1,
 TESTI20073460//1, TESTI20095200//6, TESTI20095880//10, TESTI20100090//1, TESTI20102390//2,
 5 TESTI20113940//3, TESTI20121040//1, TESTI20149880//3, TESTI20151800//3, TESTI20162780//4,
 TESTI20170170//1, TESTI20173050//1, TESTI20186110//11, TESTI20198540//2, TESTI20199110//1,
 TESTI20202830//1, TESTI20204260//1, TESTI20214630//2, TESTI20244730//1, TESTI20245860//1,
 TESTI20246410//1, TESTI20257910//1, TESTI20260640//1, TESTI20261040//4, TESTI20262150//11,
 TESTI20262940//1, TESTI20264910//1, TESTI20271790//9, TESTI20278280//3, TESTI20282420//2,
 10 TESTI20282900//1, TESTI20286590//1, THYMU20007020//3, THYMU20012020//1, THYMU20017270//2,
 THYMU20020800//4, THYMU20025480//3, THYMU20030690//7, THYMU20034790//2, THYMU20046350//1,
 THYMU20050010//5, THYMU20054800//2, THYMU20055740//1, THYMU20062770//1, THYMU20078240//1,
 THYMU20079690//2, THYMU20083390//3, THYMU20087270//1, THYMU20100940//4, THYMU20106990//1,
 THYMU20115380//2, THYMU20137050//3, THYMU20137570//1, THYMU20143230//2, THYMU20145990//3,
 15 THYMU20150190//2, THYMU20153210//10, THYMU20154790//3, THYMU20163600//2, THYMU20171580//1,
 THYMU20176010//1, THYMU20178440//1, THYMU20185470//2, TRACH20011540//2, TRACH20021380//4,
 TRACH20073990//1, TRACH20081270//2, TRACH20149720//1, TRACH201497401//1, TRACH20163470//11,
 TRACH20165330//3, TRACH20167090//2, TRACH20173680//8, UMVEN10001380//2, UTERU20035770//1,
 UTERU20045200//5, UTERU20064120//7, UTERU20086530//2, UTERU20089300//1, UTERU20095100//3,
 20 UTERU20099040//5, UTERU20103200//3, UTERU20125810//1, UTERU20127150//8, UTERU20139760//1,
 UTERU20188840//2

[0223] The Names of clones whose deduced amino acid sequences were detected to have functional domains with Pfam, and the name of hit functional domains are as follows. The search result is indicated as "clone name//functional domain name". When the clone has multiple hit functional domains, they are listed and demarcated by a double slash mark (/). When the clone has multiple hits of an identical functional domain, each is listed without abridgment.

ADRGL20020290//Sodium:galactoside symporter family//Nucleoside transporter ADRGL20021910//Immunoglobulin domain

ADRGL20026790//PWWP domain

ADRGL20036840//Class I Histocompatibility antigen, domains alpha 1 and 2

30 ADRGL20047770//ATP synthase (F14-kDa) subunit

ADRGL20059610//O-Glycosyl hydrolase family 30

ADRGL20062330//Spectrin repeat//Spectrin repeat//Bacterial flagellin N-terminus//Spectrin repeat//Spectrin repeat//Spectrin repeat

ADRGL20066770//Collagen triple helix repeat (20 copies)//C1q domain

35 ADRGL20079060//Transglutaminase-like superfamily

ASTRO20006530//Intermediate filament proteins//Myc leucine zipper domain

ASTRO20010010//Photosynthetic reaction center protein

ASTRO20010290//PHD-finger

40 ASTRO20026320//Viral (Superfamily 1) RNA helicase//Heavy-metal-associated domain//Viral (Superfamily 1) RNA helicase

ASTRO20038400//Homeobox domain//Common central domain of tyrosinase//Rhabdovirus nucleocapsid protein//Homeobox domain//Homeobox domain//Homeobox domain

ASTRO20046280//MutT-like domain

ASTRO20050810//FGGY family of carbohydrate kinases//FGGY family of carbohydrate kinases

45 ASTRO20052420//RhoGEF domain//PH domain//SH3 domain

ASTRO20053430//FERM domain (Band 4.1 family)//FERM domain (Band 4.1 family)//Delta-aminolevulinic acid dehydratase//Lipoprotein amino terminal region

ASTRO20055570//Prion protein

ASTRO20055930//Aldehyde oxidase and xanthine dehydrogenase, C terminus//Zinc finger, C3HC4 type (RING finger)

50 ASTRO20085080//WD domain, G-beta repeat//Fibrillarin//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

ASTRO20088950//Glycosyl hydrolase family 1

BGGI120010750//Phosphoglucose isomerase//Ribosomal protein L7Ae

BNGH420015760//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

55 BNGH420024870//C2 domain//C2 domain//C2 domain

BNGH420035290//Zinc finger, C3HC4 type (RING finger)//TRAF-type zinc finger//Hr1 repeat motif//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
BNGH420036410//Arsenical pump membrane protein
BNGH420046790//Immunoglobulin domain
BNGH420052350//Urotensin II
5 BNGH420059680//NHL repeat//NHL repeat//NHL repeat//NHL repeat
BNGH420070370//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
finger, C2H2 type
BNGH420074600//RNA polymerase beta subunit
BNGH420077980//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin do-
10 main//Immunoglobulin domain//Immunoglobulin domain
BNGH420086030//PH domain//RhoGAP domain
BRACE20003310//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
15 BRACE20007330//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
BRACE20014450//alpha/beta hydrolase fold
BRACE20050870//DEAD/DEAH box helicase
BRACE20051600//Reverse transcriptase (RNA-dependent DNA polymerase)
BRACE20051930//MAM domain.
20 BRACE20054600//von Willebrand factor type D domain
BRACE20055560//WD domain, G-beta repeat//WD domain, G-beta repeat
BRACE20059810//TSC-22/dip/bun family
BRACE20061620//SPRY domain
BRACE20065470//Ubiquitin family
25 BRACE20069000//CLN3 protein
BRACE20079200//von Willebrand factor type D domain
BRACE20099070//FYVE zinc finger
BRACE20196180//HMG (high mobility group) box
BRACE20204670//Protein-tyrosine phosphatase//Dual specificity phosphatase, catalytic domain//Fatty acid desatu-
30 rase//Protein-tyrosine phosphatase
BRACE20215410//Imidazoleglycerol-phosphate dehydratase//UvrD/REP helicase
BRAMY20001510//Zinc finger, C3HC4 type (RING finger)//PHD-finger
BRAMY20003540//PH domain//EF hand//EF hand//Viral RNA dependent RNA polymerase//Phosphatidylinositol-spe-
cific phospholipase C, X domain//Phosphatidylinositol-specific phospholipase C, Y domain//Bleomycin resistance pro-
35 tein//C2 domain
BRAMY20005080//Ubiquitin carboxyl-terminal hydrolase family 2
BRAMY20013670//S-adenosylmethionine synthetase
BRAMY20016780//Proprotein convertase P-domain
BRAMY20023640//UBX domain
40 BRAMY20027990//C2 domain
BRAMY20028620//Quinolinate phosphoribosyl transferase
BRAMY20035380//Cation efflux family
BRAMY20035830//BTB/POZ domain//Thymidylate synthase
BRAMY20038980//Granulocyte-macrophage colony-stimulating factor//Borrelia outer surface protein E and F
45 BRAMY20040580//Zinc finger, C2H2 type//Zinc finger, C2H2 type
BRAMY20043630//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine
Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich
Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
BRAMY20044920//Ubiquitin carboxyl-terminal hydrolase family 2
50 BRAMY20045420//Domain found in Dishevelled, Egl-10, and Pleckstrin
BRAMY20051820//C2 domain
BRAMY20056620//Ca transferase domain
BRAMY20056840//PWWP domain
BRAMY20076100//Ligand-binding domain of nuclear hormone receptor
55 BRAMY20089770//ATP P2X receptor
BRAMY20091230//Mitochondrial carrier proteins//Mitochondrial carrier proteins
BRAMY20094890//SURF4 family
BRAMY20102900//Ephrin

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[illegible]

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[illegible]

CTONG20184830//ABC transporter
CTONG20186290//Aldehyde dehydrogenase family
CTONG20186370//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20186520//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
CTONG20186550//BTB/POZ domain//K+ channel tetramerisation domain
CTONG20188080//TPR Domain
CTONG20189000//RhoGEF domain
CTONG20190290//R3H domain//RNA dependent RNA polymerase//Uncharacterized protein family UPF0024
DFNES20025500//Sigma-54 interaction domain//ATPases associated with various cellular activities (AAA)
DFNES20043710//Src homology domain 2//Domain of unknown function DUF36
DFNES20055400//Viral coat protein//Putative diphthamide synthesis protein//Influenza non-structural protein (NS1)
DFNES20057660//Plant thionins//Mitochondrial carrier proteins//Mitochondrial carrier proteins
DFNES20072990//Integral membrane protein DUF6//Integral membrane protein DUF6
DFNES20073320//Zinc finger, C3HC4 type (RING finger)//PHD-finger//B-box zinc finger.
DFNES20076340//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
DFNES20080880//Glycosyl transferases//Similarity to lectin domain of ricin beta-chain, 3 copies.
DFNES20094820//PHD-finger//Zn-finger in ubiquitin-hydrolases and other proteins
FCBBF10000230//Sec7 domain//PH domain
FCBBF10004760//HMG (high mobility group) box
FCBBF20018680//C2 domain//C2 domain
FCBBF20020440//Urease
FCBBF20023490//Helicases conserved C-terminal domain
FCBBF20033360//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
FCBBF20035430//AN1-like Zinc finger//AN1-like Zinc finger
FCBBF20035490//KH domain
FCBBF20041380//SAM domain (Sterile alpha motif)
FCBBF20043730//UBA domain
FCBBF20059660//TPR Domain
FCBBF20066340//PH domain
FCBBF20070950//DNA binding domain with preference for A/T rich regions
FCBBF30001100//DENN (AEX-3) domain//PPR repeat
FCBBF30002270//linker histone H1 and H5 family
FCBBF30003610//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Plant PEC family metallothionein//DM DNA binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Phorbol esters/diacylglycerol binding domain (C1 domain)
FCBBF30004340//Ribosomal protein S3, C-terminal domain./Similarity to lectin domain of ricin beta-chain, 3 copies.
FCBBF30005360//Sigma-54 interaction domain//ATPases associated with various cellular activities (AAA)//ATPases associated with various cellular activities (AAA)
FCBBF30005500//PH domain//PH domain//Putative GTP-ase activating protein for Arf
FCBBF30019140//'chromo' (CHRromatin Organization Modifier) domain/'chromo' (CHRromatin Organization Modifier) domain//DEAD/DEAH box helicase//SNF2 and others N-terminal domain//Helicases conserved C-terminal domain
FCBBF30019180//Armadillo/beta-catenin-like repeats//Lipoprotein amino terminal region
FCBBF30021900//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//BolA-like protein//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Snake toxin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type FCBBF30022680//3'-5' exonuclease
FCBBF30029250//SET domain
FCBBF30035570//C2 domain
FCBBF30048420//T-box//wnt family of developmental signaling proteins
FCBBF30071500//Influenza RNA-dependent RNA polymerase subunit PB1//Reprolysins family propeptide//Leptin
FCBBF30076310//Eukaryotic protein kinase domain//Eukaryotic protein kinase domain//Protein kinase C terminal domain

FCBBF30079770//D-isomer specific 2-hydroxyacid dehydrogenases
FCBBF30080730//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//Zinc knuckle
FCBBF30085560//Pyridine nucleotide-disulphide oxidoreductase//FAD binding domain//Flavin containing amine ox-
idase//Phytoene dehydrogenase related enzyme
5 FCBBF30093170//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
finger, C2H2 type
FCBBF30100080//Sec7 domain
FCBBF30100120//PD2 domain (Also known as DHR or GLGF).
FCBBF30100410//Nucleosome assembly protein (NAP)
10 FCBBF30118670//Reprolysins (M12B) family zinc metalloprotease//Disintegrin//EB module//Hantavirus glycoprotein
G2//Adenovirus E3 region protein CR2//jmiN domain
FCBBF30125460//Zinc finger, C3HC4 type (RING finger)
FCBBF30129010//KRAB box//Zinc finger, C2H2 type//GATA zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2
type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type
15 FCBBF30130410//UvrB/uvrC motif
FCBBF30132050//Galactosyltransferase//Fringe-like
FCBBF30132660//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich
Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
FCBBF30136230//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//
20 Cystatin domain//Homeobox domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
FCBBF30142290//PHD-finger
FCBBF30143550//Phosphatidylinositol-4-phosphate 5-Kinase
FCBBF30153170//Phosphofructokinase//Phosphofructokinase//Phosphofructokinase
FCBBF30161780//gag gene protein p24 (core nucleocapsid protein)//Zinc knuckle
25 FCBBF30164510//Cadherin domain//Cadherin domain//Cadherin domain//Fructose-bisphosphate aldolase class-I/
Cadherin domain//Cadherin domain//Alphaherpesvirus glycoprotein E//Cadherin cytoplasmic region
FCBBF30166220//Serine hydroxymethyltransferase
FCBBF30169280//PHD-finger//Zinc finger, C3HC4 type (RING finger)
FCBBF30171230//Subtilase family//Proprotein convertase P-domain
30 FCBBF30173960//Beta-lactamase//TPR Domain
FCBBF30194550//Arsenical pump membrane protein//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//
Dehydrogenase E1 component//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat
FCBBF30195690//C2 domain
FCBBF30197840//Sushi domain (SCR repeat)//CUB domain//Sushi domain (SCR repeat)//CUB domain//Sushi domain
35 (SCR repeat)//Sushi domain (SCR repeat)//Sushi domain (SCR repeat)
FCBBF30212210//Immunoglobulin domain
FCBBF30215240//PH domain//FERM domain (Band 4.1 family)
FCBBF30220050//Ligand-binding domain of nuclear hormone receptor
FCBBF30222910//Corticotropin-releasing factor family
40 FCBBF30236670//DEAD/DEAH box helicase
FCBBF30250980//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain,
G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
FCBBF30255680//Vesicular monoamine transporter//GGL domain//Ezrin/radixin/moesin family//Ank repeat//Ank re-
peat
45 FCBBF30257370//Gemini virus AL1 protein//Outer membrane efflux protein
FCBBF30259050//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger present in dys-
trophin, CBP/p300//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//DM DNA bind-
ing domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcrip-
tion factor S-II (TFIIS)//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//
50 Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
FCBBF30260210//SNF2 and others N-terminal domain//Helicases conserved C-terminal domain//Domain of unknown
function DUF94
FCBBF30263080//Zinc finger, C2H2 type//Zinc finger, C2H2 type
FCBBF30266510//Domain of unknown function DUF71
55 FCBBF30271990//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//
Ank repeat//Ank repeat//Ank repeat//Ank repeat
FCBBF30275590//LIM domain containing proteins
FCBBF30282020//Ank repeat//Ank repeat//Ank repeat//K+ channel tetramerisation domain//BTB/POZ domain

- FCBBF30285930//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- FCBBF50001650//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif
- 5 FCBBF50003530//Zinc finger, C3HC4 type (RING finger)
- FCBBF50004950//Putative replicase 1 (ORF2)
- FEBRA20005040//Intermediate filament proteins//Hr1 repeat motif//Troponin//GrpE
- FEBRA20007820//DNA polymerase family B
- FEBRA20018670//Viral methyltransferase//Riboso protein 519//Alpha-2-macroglobulin family N-terminal region
- 10 FEBRA20026820//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recogin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- FEBRA20027070//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- 15 FEBRA20029620//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
- FEBRA20031000//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Insulin/IGF/Relaxin family//Ribosomal RNA adenine dimethylases//SAM domain
- 20 (Sterile alpha motif)//TFII E alpha subunit//Zinc finger, C3HC4 type (RING finger)
- FEBRA20031280//Protein of unknown function DUF82
- FEBRA20038330//Corticotropin-releasing factor family
- FEBRA20038970//Laminin EGF-like (Domains III and V)//Pho esters/diacylglycerol binding domain (C1 domain)//EGF-like domain//EGF-like domain//Trypsin Inhibitor like cysteine rich domain//Metallothionein//EGF-like domain//EGF-like domain//Extracellular link domain
- 25 FEBRA20046200//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat
- FEBRA20046510//Zinc finger, C2H2 type//Zinc finger, C2H2 type//BolA-like protein//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- 30 FEBRA20063720//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- 35 FEBRA20078800//NADH ubiquinone oxidoreductase, 20 Kd subunit
- FEBRA20080860//Hantavirus glycoprotein G2
- FEBRA20087550//WD domain, G-beta repeat//WD domain, G-beta repeat
- FEBRA20088610//CRAL/TRIO domain.
- FEBRA20088810//Fibroblast growth factor
- 40 FEBRA20090160//Nuclear transition protein 2
- FEBRA20090220//Nucleotidyl transferase//Bacterial transferase hexapeptide (four repeats)//Bacterial transferase hexapeptide (four repeats)//Bacterial transferase hexapeptide (four repeats)//Domain of unknown function DUF29//Peptide hormone//eIF4-gamma/eIF5/eIF2-epsilon
- FEBRA20092760//LIM domain containing proteins//LIM domain containing proteins//LIM domain containing proteins
- 45 FEBRA20115930//Divalent cation transporter//Translation initiation factor IF-3//Divalent cation transporter
- FEBRA20150420//Transient receptor//Borrelia ORF-A//Transient receptor
- FEBRA20170240//SCAN domain//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- FEBRA20172230//Phospholipase D. Active site motif//Phospholipase D. Active site motif
- 50 FEBRA20173330//Eukaryotic protein kinase domain
- FEBRA20175330//D-isomer specific 2-hydroxyacid dehydrogenases
- FEBRA20191720//GGL domain//Regulator of G protein signaling domain
- HCHON10000150//LIM domain containing proteins//LIM domain containing proteins//LIM domain containing proteins//Zinc finger, C3HC4 type (RING finger)
- 55 HCHON20000870//Eukaryotic protein kinase domain
- HCHON20002650//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- HCHON20002710//Ubiquitin carboxyl-terminal hydrolase family 2
- HCHON20015050//von Willebrand factor type A domain//IPT/TIG domain//Sm protein

HEART10001420//MYND finger//SET domain
HEART10001490//FAD binding domain
HEART20009590//Peptidase family M41
HEART20019310//Zinc finger, C3HC4 type (RING finger)//PHD-finger//B-box zinc finger.
5 HEART20022200//Influenza Matrix protein (M1)//metallopeptidase family M24
HEART20047640//3'5'-cyclic nucleotide phosphodiesterase//Formin Homology 2 Domain
HEART20082570//C-5 cytosine-specific DNA methylase//Glycine cleavage T-protein (aminomethyl transferase)
HHDPC20081230//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM,
RBD, or RNP domain)//RNA recognition motif. (a. k. a. RRM, RBD, or RNP domain)//RNA recognition motif. (a. k. a.
10 RRM, RBD, or RNP domain)
HHDPC20088160//PDZ domain (Also known as DHR or GLGF).
HLUNG20008460//bZIP transcription factor
HLUNG20011260//Eukaryotic protein kinase domain
HLUNGZOO11460//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM,
15 RBD, or RNP domain)
HLUNG20014590//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recogin//Zinc finger, C2H2
type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
20 HLUNG20015070//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich
Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat
C-terminal domain//Immunoglobulin domain
HLUNG20024050//Rubredoxin
HLUNG20028110//Zinc finger, C3HC4 type (RING finger)//TPR Domain//TPR Domain//TPR Domain//Zinc finger,
C3HC4 type (RING finger)//Aldo/keto reductase family
25 HLUNG20030420//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat
HLUNG20032460//Pro oligopeptidase family//Lipoate-protein ligase B//alpha/beta hydrolase fold
HLUNG20033060//HMG (high mobility group) box
HLUNG20041590//TPR Domain//TPR Domain//Domain of unknown function DUF27
HLUNG20042730//Cytochrome P450
30 HLUNG20051330//FHIPEP family
HLUNG20063700//Progesterone receptor
HLUNG20065990//bZIP transcription factor//SNAP-25 family//Syntaxin
HLUNG20068120//Fimbrin Usher proteins
HLUNG20069350//EF hand//EF hand//EF hand
35 HLUNG20070410//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
HLUNG20081390//DnaJ domain
HLUNG20082350//PH domain//START domain
HLUNG20083330//DNA polymerase III beta subunit//Fibrillar collagen C-terminal domain
HLUNG20084790//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
40 HLUNG20085210//C2 domain
KIDNE20016360//PAS domain//PAC motif//Ion transport protein//Transmembrane region cyclic Nucleotide Gated
Channel//Cyclic nucleotide-binding domain KIDNE20027980//SAM domain (Sterile alpha motif)
KIDNE20080690//Glycosyl hydrolases family 18//Aminotransferases class-III pyridoxal-phosphate//Methyl-accepting
chemotaxis protein (MCP) signaling domain//Aminotransferases class-III pyridoxal-phosphate
45 KIDNE20081170//Kinesin motor domain//Kinesin motor domain
KIDNE20083620//Asparaginase
KIDNE20084030//Sugar (and other) transporter
KIDNE20084730//Neuraxin and MAP1B proteins//Formin Homology 2 Domain
KIDNE20086490//gag gene protein p24 (core nucleocapsid protein)
50 KIDNE20087880//Reverse transcriptase (RNA-dependent DNA polymerase)
KIDNE20088240//EF hand//EF hand//EF hand
KIDNE20089870//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain,
G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
KIDNE20094670//Sigma-54 interaction domain//FtsK/SpoIIIE family//ATPases associated with various cellular activi-
55 ties (AAA)
KIDNE20133880//G-protein alpha subunit
KIDNE20141700//Ribosomal family S4e
KIDNE20142900//EGF-like domain//EB module//EGF-like domain//EGF-like domain

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KIDNE20148080//Zinc finger, C3HC4 type (RING finger)
 KIDNE20149780//Ank repeat//Ank repeat//Ank repeat
 KIDNE20152440//Trypsin//PDZ domain (Also known as DHR or GLGF).
 KIDNE20154330//PDZ domain (Also known as DHR or GLGF)//PDZ domain (Also known as DHR or GLGF)//PDZ
 5 domain (Also known as DHR or GLGF)//PDZ domain (Also known as DHR or GLGF)//PDZ domain (Also known as
 DHR or GLGF)//PDZ domain (Also known as DHR or GLGF).
 KIDNE20160360//Sec7 domain//PH domain
 KIDNE20169180//EGF-like domain//EB module//EGF-like domain//Trypsin Inhibitor like cysteine rich domain//EGF-
 like domain//TNFR/NGFR cysteine-rich region//Zona pellucida-like domain
 10 KIDNE20170400//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Protein kinase C terminal do-
 main//Rubredoxin
 KIDNE20173150//Acetyltransferase (GNAT) family
 KIDNE20173430//PDZ domain (Also known as DHR or GLGF)//PDZ domain (Also known as DHR or GLGF).
 KIDNE20186170//UDP-glucuronosyl and UDP-glucosyl transferases
 15 KIDNE20189960//Trehalase
 LIVER20006260//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Plant PEC family metallothionein//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type
 LIVER20007750//Sugar (and other) transporter
 20 LIVER20010760//Lectin C-type domain
 LIVER20010990//DNA gyrase/topoisomerase IV, subunit A
 LIVER20013890//tRNA synthetases class I (C)
 LIVER20026440//Cytochrome P450
 LIVER20030650//General diffusion Gram-negative porins
 25 LIVER20038000//Mitochondrial carrier proteins//Mitochondrial carrier proteins//Mitochondrial carrier proteins
 LIVER20040740//CRAL/TRIO domain.
 LIVER20055270//AIR synthase related protein
 MESAN20006200//Annexin//Annexin
 MESAN20008150//IBR domain
 30 MESAN20009090//CUB domain
 MESAN20016270//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger,
 C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger,
 C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 MESAN20021130//SH3 domain//Eukaryotic protein kinase domain
 35 MESAN20021220//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine
 Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Leucine rich repeat N-terminal domain//
 Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leu-
 cine rich repeat C-terminal domain
 MESAN20026870//PAN domain//TBC domain
 40 MESAN20027240//RhoGEF domain
 MESAN20027900//von Willebrand factor type A domain//von Willebrand factor type A domain//von Willebrand factor
 type A domain//Protozoan/cyanobacterial globin//von Willebrand factor type A domain//von Willebrand factor type A
 domain
 MESAN20030350//LGN motif, putative GEF specific for G-alpha GTPase//DNA gyrase/topoisomerase IV, subunit A
 45 MESAN20030370//Porphobilinogen deaminase//GHMP kinases putative ATP-binding proteins//Protein of unknown
 function DUF113
 MESAN20034440//Viral DNA-binding protein//Uncharacterized protein family UPF0024
 MESAN20038520//Caspase recruitment domain//RNA polymerase beta subunit
 MESAN20057240//Elongation factor TS//Helix-hairpin-helix motif.
 50 MESAN20058110//FKBP-type peptidyl-prolyl cis-trans isomerases//Elongation factor Tu family//FKBP-type peptidyl-
 prolyl cis-trans isomerases//FKBP-type peptidyl-prolyl cis-trans isomerases
 MESAN20059570//EGF-like domain//SEA domain//Immunoglobulin domain
 MESAN20060430//SET domain
 MESAN20067430//Tropomyosins
 55 MESAN20069530//Calponin homology (CH) domain//PDZ domain (Also known as DHR or GLGF).
 MESAN20090190//EGF-like domain//EGF-like domain//EGF-like domain//EGF-like domain//EGF-like domain//EGF-
 like domain//Metallothionein//CUB domain
 MESAN20095220//Adaptin N terminal region

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tion factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 NTONG20005310//Ribosomal protein S9/S16
 NTONG20029850//EF hand//EF hand//EF hand
 NTONG20031580//Hsp20/alpha crystallin family
 5 NTONG20032100//Intermediate filament proteins
 NTONG20034540//GAF domain//GAF domain//3'5'-cyclic nucleotide phosphodiesterase
 NTONG20035150//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
 NTONG20043080//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
 NTONG20048440//PH domain//K-box region
 10 NTONG20053630//DNA binding domain with preference for A/T rich regions//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Progesterone receptor//Zinc finger, C2H2 type
 NTONG20053730//Ribosomal protein S2//Ubiquitin carboxyl-terminal hydrolases family 2//Ubiquitin carboxyl-terminal
 hydrolase family 2
 NTONG20053910//Translin family//PH domain//Putative GTP-ase activating protein for Arf//Ank repeat//Ank repeat
 15 NTONG20055200//Calcium channel extracellular region//Elongation factor Tu family//Elongation factor G C-terminus
 NTONG20058010//AMP-binding enzyme
 OCBBF20000740//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich
 Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Immunoglobulin domain
 OCBBF20011860//LIM domain containing proteins
 20 OCBBF20012520//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich
 Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine rich repeat C-terminal domain//Immunoglobulin domain
 OCBBF20016390//Chitin synthase//Fibronectin type II domain
 OCBBF20016810//Paired box' domain
 OCBBF20110210//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
 25 OCBBF20113110//AP endonuclease family 1
 OCBBF20116250//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type
 OCBBF20120010//Thrombospondin type 1 domain
 OCBBF20120950//K+ channel tetramerisation domain//BTB/POZ domain//Zinc finger, C2H2 type//Zinc finger, C2H2
 30 type
 OCBBF20121910//Ribosomal protein L24e
 OCBBF20147070//DNA polymerase (viral) C-terminal domain
 OCBBF20156450//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger, C2H2 type
 35 OCBBF20157970//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//DM
 DNA binding domain//Zinc finger, C2H2 type
 OCBBF20165910//DnaB-like helicase
 OCBBF20166890//CAP-Gly domain//CAP-Gly domain
 40 OCBBF20166900//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II
 (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 OCBBF20167290//haloacid dehalogenase-like hydrolase//Thioredoxin//Aminoglycoside phosphotransferase//
 Acyl-CoA dehydrogenase
 OCBBF20174580//Cyclin
 45 OCBBF20174890//Death domain
 OCBBF20175360//Zinc finger, C2H2 type
 OCBBF20177540//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Src homology
 domain 2//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 OCBBF20177910//Corticotropin-releasing factor family
 50 OCBBF20182060//Inward rectifier potassium channel
 OCBBF20191950//EGF-like domain//Low-density lipoprotein receptor domain class A//Low-density lipoprotein recep-
 tor domain class A//EGF-like domain//Low-density lipoprotein receptor domain class A//EGF-like domain//Low-density
 lipoprotein receptor domain class A//Low-density lipoprotein receptor domain class A//EGF-like domain//EGF domain//
 Low-density lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat class B//Low-density lipopro-
 55 tein receptor repeat class B//Low-density lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat
 class B//EGF-like domain//60Kd inner membrane protein
 PANCR10000860//Trypsin//Trypsin
 PEBLM10001470//Zinc finger, C2H2 type//Fork head domain

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- PEBLM20001800//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
- PEBLM20003260//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Src homology domain 2//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Src homology domain 2//Zinc finger, C2H2 type
- 5 PEBLM20005020//Virion host shutoff protein
- PLACE50001390//PHD-finger
- PLACE60004260//Cystatin domain
- PLACE60006300//Immunoglobulin domain
- PLACE60012620//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
- 10 PLACE60054230//C methyltransferase//Formin Homology 2 Domain
- PLACE60054820//Regulator of chromosome condensation (RCC1)//Regulator of chromosome condensation (RCC1)
- PLACE60054870//IQ calmodulin-binding motif//IQ calmodulin-binding motif
- 15 PLACE60055590//Zinc finger, C3HC4 type (RING finger)
- PLACE60061370//Phosphotyrosine interaction domain (PTB/PID)//Extracellular link domain
- PLACE60062660//Gamma-adaptin, C-terminus
- PLACE60064180//Lumenal portion of Cytochrome b559, alpha (gene psbE) subunit//Viral (Superfamily 1) RNA helicase
- 20 PLACE60066970//SCAN domain//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- PLACE50070500//Immunoglobulin domain//Immunoglobulin domain
- PLACE60073090//Myo-inositol-1-phosphate synthase
- PLACE60074820//Adenylate kinase
- 25 PLACE60082850//Pathogenesis-related protein Bet v I family
- PLACE60087680//Thyroglobulin type-1 repeat
- PLACE60093380//Penicillin amidase//Bacterial regulatory proteins, lacI family//Vacuolar sorting protein 9 (VPS9) domain
- PLACE60095600//DEAD/DEAH box helicase
- 30 PLACE60098350//MAGE family
- PLACE60104fi30//Photosystem I reaction centre subunit VIII
- PLACE60113340//EGF-like domain//Laminin G domain//Insulin-like growth factor binding proteins//EGF-like domain//Laminin G domain
- PLACE60118810//bZIP transcription factor//TPR Domain//TPR Domain//TPR Domain//TPR Domain//PPR repeat
- 35 PLACE64119700//EF hand
- PLACE60122970//Zinc finger, C2H2 type
- PLACE60138840//Syndecan domain//Mitochondrial carrier proteins//Mitochondrial carrier proteins//Mitochondrial carrier proteins
- PLACE60140640//Phosphoribulokinase//Shikimate kinase//Uncharacterized protein family UPF0038
- 40 PLACE60154450//RhoGAP domain
- PLACE60177880//Immunoglobulin domain//Immunoglobulin domain
- PLACE60181870//Pentaxin family
- PLACE60184870//LBP / BPI / CETP family
- PROST10001100//Keratin, high sulfur B2 protein
- 45 PROST20007170//KRAB box//Zinc finger, C2H2 type//Cyclopropane-fatty-acyl-phospholipid synthase//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- PROST20015210//Myosin tail//Borrelia lipoproteins//Myosin tail
- PROST20016760//'chromo' (CHRromatin Organization Modifier) domain
- 50 PROST20024250//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- PROST20028970//Ank repeat//Ank repeat//Glutamine amidotransferases class-II//Ank repeat//Ank repeat
- PROST20033240//Ephrin receptor ligand binding domain//EB module//TNFR/NGFR cysteine-rich region//Fibronectin type III domain
- PROST20036350//Glutathione S-transferases//Ribosomal protein S24e//Interferon alpha/beta domain//tRNA synthetases class I (E and Q)
- 55 PROST20045700//Keratin, high sulfur B2 protein
- PROST20050390//Cytochrome P450
- PROST20051310//DEAD/DEAH box helicase//Toprim domain//Helicases conserved C-terminal domain//Zinc knuckle

PROST20065790//Phosphofructokinase//Phosphofructokinase//Phosphofructokinase//Phosphofructokinase
PROST20073280//Transposase
PROST20075280//Immunoglobulin domain//Immunoglobulin domain//Thrombospondin type 1 domain
PROST20082430//Cyclophilin type peptidyl-prolyl cis-trans isomerase
5 PROST20084720//Cytochrome P450
PROST20087240//gag gene protein p24 (core nucleocapsid protein)
PROST20099090//Disintegrin
PROST20102190//EF hand//Ribosomal RNA adenine dimethylases//EF hand
PROST20105450//Sodium/hydrogen exchanger family
10 PROST20127450//TSC-22/dip/bun family
PROST20130320//S-100/ICaBP type calcium binding domain
PROST20152510//TPR Domain//TPR Domain//TPR Domain
PROST20155370//SCAN domain//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//
Zinc finger, C2H2 type//Zinc finger, C2H2 type
15 PROST20168600//KTN NAD-binding domain
FUAEN10000650//TSC-22/dip/bun family
PUAEN10001640//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
PUAEN20000800//Bleomycin resistance protein
PUAEN20001520//Acetyltransferase (GNAT) family
20 PUAEN20002470//FtsK/SpoIIIE family
PUAEN20003120//Myb-like DNA-binding domain//ATP synthase ab C terminal//SET domain
SALGL10001070//Family 4 glycosyl hydrolase
SKMUS20006790//von Willebrand factor type D domain
SKMUS20007260//Syndecan domain
25 SKMUS20008730//Calponin homology (CH) domain
SKMUS20017400//Hantavirus nucleocapsid protein//Tropomyosins
SKMUS20040440//Ribosomal protein L3
SKMUS20091900//Trypsin
SKNMC10001230//Ank repeat//Ank repeat//Ank repeat
30 SKNMC20006350//FKBP-type peptidyl-prolyl cis-trans isomerases//FKBP-type peptidyl-prolyl cis-trans isomerases//
FKBP-type peptidyl-prolyl cis-trans isomerases//EF hand//EF hand
SKNSH20009710//Tropomyosins//Tropomyosins
SKNSH20052400//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain,
G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
35 SKNSH20057920//Eukaryotic protein kinase domain
SMINT20000070//Rabphilin-3A effector domain
SMINT20002320//Protein phosphatase 2A regulatory B subunit (B56 family)
SMINT20006020//PH domain//Phor esters/diacylglycerol binding domain (C1 domain)//FYVE zinc finger//PH domain
SMINT20006090//Glutathione S-transferases.
40 SMINT20008110//Na+/K+ ATPase C-terminus
SMINT20011950//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
type//PHD-finger//Zinc finger, C2H2 type
SMINT20012220//Collagen triple helix repeat (20 copies)
SMINT20016150//gag gene protein p17 (matrix protein).//Ferritins
45 SMINT20024140//Immunoglobulin domain
SMINT20028800//Zinc finger, C2HC type//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain
SMINT20028840//Immunoglobulin domain
SMINT20030740//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
50 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
type//Zinc finger, C2H2 type
SMINT20035050//SH3 domain//WW domain//PH domain//RhoGAP domain
SMINT20036440//ENTH domain
SMINT20038660//Olfactomedin-like domain
55 SMINT20039050//Flavivirus glycoprotein//IBR domain
SMINT20043390//Ras association (RalGDS/AF-6) domain
SMINT20044140//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type

SMINT20044730//Envelope glycoprotein GP120
 SMINT20048720//Cytochrome P450//Cytochrome P450
 SMINT20052130//Ank repeat//Ank repeat
 SMINT20056230//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin do-
 5 main
 SMINT20062050//Reverse transcriptase (RNA-dependent DNA polymerase)
 SMINT20077960//Gelsolin repeat//Gelsolin repeat//Gelsolin repeat//Gelsolin repeat.
 SMINT20083290//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin do-
 main//Immunoglobulin domain
 10 SMINT20086250//Glycine cleavage H-protein
 SMINT20086720//SCAN domain//KRAB box
 SMINT20088440//Immunoglobulin domain
 SMINT20089600//PDZ domain (Also known as DHR or GLGF).
 SMINT20091190//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin do-
 15 main//Immunoglobulin domain
 SPLEN20006950//Reverse transcriptase (RNA-dependent DNA polymerase)
 SPLEN20011350//Helper component proteinase
 SPLEN20015100//DHHC zinc finger domain
 SPLEN20023540//RasGEF domain//EF hand//EF hand
 20 SPLEN20023850//RecF protein//SMC domain N terminal domain//Tropomyosins
 SPLEN20024190//EGF-like domain//EB module//EGF-like domain//Trypsin Inhibitor like cysteine rich domain//EGF-
 like domain//EGF-like domain//WAP-type (Whey Acidic Protein) 'four-disulfide core'/EGF-like domain
 SPLEN20024930//inosi polyphosphate phosphatase family, catalytic domain
 SPLEN20039180//Fatty acid desaturase
 25 SPLEN20042200//Zinc finger, C3HC4 type (RLNG finger)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger,
 C2H2 type//Zinc finger, C2H2 type
 SPLEN20049840//Polyphosphate kinase//Myosin head (motor domain)//IQ calmodulin-binding motif//SH3 domain
 SPLEN20050090//Pyridoxamine 5'-phosphate oxidase//GRIP domain
 SPLEN20054500//Renal dipeptidase
 30 SPLEN20055600//K+ channel tetramerisation domain//BTB/POZ domain//Zinc finger, C2H2 type
 SPLEN20057900//Scorpion short toxins//EGF-like domain//EGF-like domain//Keratin, high sulfur B2 protein
 SPLEN20059270//Zinc finger, C3HC4 type (RING finger)//B-box zinc finger//SPRY domain
 SPLEN20063250//Zinc finger, C2H2 type
 SPLEN20063890//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine
 35 Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
 SPLEN20071820//DNA polymerase X family
 SPLEN20076470//TPR Domain//TPR Domain//TPR Domain
 SPLEN20080070//Alpha-L-fucosidase
 SPLEN20085910//Double-stranded RNA binding motif
 40 SPLEN20090880//Immunoglobulin domain
 SPLEN20098030//Zinc finger, C3HC4 type (RING finger)//B-box zinc finger.
 SPLEN20101950//Sodium/hydrogen exchanger family
 SPLEN20104150//Ribosomal protein L36
 SPLEN20108000//short chain dehydrogenase
 45 SPLEN20110180//Transposase
 SPLEN20118050//Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich
 Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
 SPLEN20135030//PDZ domain (Also known as DHR or GLGF).//GATA zinc finger//LIM domain containing proteins
 SPLEN20139100//Sodium and potassium ATPases//Immunoglobulin domain//Immunoglobulin domain//Immunoglob-
 50 ulin domain//Immunoglobulin domain
 SPLEN20139360//Bacterial regulatory proteins, lacI family//Site-specific recombinases
 SPLEN20175920//Uncharacterized protein family UPF0036
 SPLEN20180980//Glutathione S-transferases.
 SPLEN20182990//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch motif
 55 SPLEN20183020//Laminin G domain
 SPLEN20191020//Src homology domain 2
 SPLEN20193790//Dynamin family//Dynamin family//Proteasome activator pa28 beta subunit//Peroxidase//Dynamin
 central region//Dynamin GTPase effector domain SPLEN20195710//TPR Domain//TPR Domain//TPR Domain

SPLEN20197930//K-box region
 SPLEN20198390//WD domain, G-beta repeat//Fibrillarin//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 SPLEN20201830//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
 5 TESTI10001570//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type
 10 TESTI20006160//Large-conductance mechanosensitive channel, MscL//CbiM
 TESTI20006830//PWFP domain
 TESTI20012080//Chitin synthase
 TESTI20016970//TPR Domain
 TESTI20030200//Double-stranded RNA binding motif//Adenosine-deaminase (editase) domain//Adenosine-deaminase (editase) domain
 15 TESTI20030440//Plant PEC family metallothionein//Tropomyosins
 TESTI20031310//Serpins (serine protease inhibitors)
 TESTI20038240//Peptidase family M13
 TESTI20041630//Outer membrane efflux protein//Intermediate filament proteins
 20 TESTI20043910//IQ calmodulin-binding motif//IQ calmodulin-binding motif//IQ calmodulin-binding motif//IQ calmodulin-binding motif//IQ calmodulin-binding motif
 TESTI20045390//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
 TESTI20046110//Extracellular link domain
 25 TESTI20046490//LIM domain containing proteins//Somatomedin B domain
 TESTI20046870//CRAL/TRIO domain//CRAL/TRIO domain//MSP (Major sperm protein) domain
 TESTI20046890//PHD-finger
 TESTI20049060//Immunoglobulin domain
 TESTI20049410//Proprotein convertase P-domain
 30 TESTI20050720//Coenzyme A transferase//Alpha-2-macroglobulin family N-terminal region//Coenzyme A transferase
 TESTI20051730//Glutamine amidotransferases class-II//alpha/beta hydrolase fold
 TESTI20053070//WD domain, G-beta repeat//WD domain, G-beta repeat
 TESTI20053950//IQ calmodulin-binding motif
 TESTI20055880//Serum amyloid A protein
 35 TESTI20056030//Myosin tail
 TESTI20057430//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 TESTI20057590//Leucine rich repeat C-terminal domain//Immunoglobulin domain
 40 TESTI20057840//SAP domain//Zinc knuckle//Zinc finger, C3HC4 type (RING finger)
 TESTI20057880//Zinc finger, C3HC4 type (RING finger)
 TESTI20058350//Polyomavirus coat protein//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 TESTI20058920//Tubulin/FtsZ family
 45 TESTI20059080//Thermophilic metalloprotease (M29)//Hyaluronidase
 TESTI20059480//Cyclic nucleotide-binding domain
 TESTI200598101//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//DM DNA binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//BoIA-like protein//Zinc finger, C2H2 type//Coronavirus M matrix/glycoprotein//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 50 TESTI20060350//bZIP transcription factor
 TESTI20060830//IZAP domain//Ferric uptake regulator family//Peptidase family M1//Piwi domain
 TESTI20061090//Keratin, high sulfur B2 protein
 TESTI20061200//Sugar (and other) transporter
 55 TESTI20064370//TPR Domain//TPR Domain//TPR Domain//TPR Domain//Synaptobrevin
 TESTI20064530//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 TESTI20064650//Myosin head (motor domain)

- TESTI20065650//G-protein alpha subunit
 TESTI20066150//Picornavirus 2B protein//Glutamine amidotransferase class-I//Pancreatic hormone peptides
 TESTI20066330//Fibronectin type III domain
 TESTI20066650//RasGEF domain
 5 TESTI20067480//KRAB box//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//FYVE zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 TESTI20068530//Zinc finger, C3HC4 type (RING finger)//PHD-finger
 10 TESTI20071130//ATP synthase Alpha chain, C terminal
 TESTI20071630//Glutamine synthetase//SCP-like extracellular protein
 TESTI20075240//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recognin//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 15 TESTI20076570//Dual specificity phosphatase, catalytic domain
 TESTI20079220//KRAB box//Myb-like DNA-binding domain//Myb-like DNA-binding domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 20 TESTI20079980//PDZ domain (Also known as DHR or GLGF).//Domain found in Dishevelled, Egl-10, and Pleckstrin
 TESTI20081890//PDZ domain (Also known as DHR or GLGF).
 TESTI20084250//Oxysterol-binding protein
 TESTI20086840//von Willebrand factor type A domain
 TESTI20088840//Zinc finger, C3HC4 type (RING finger)//PHD-finger//Thymidine kinases//E7 protein, Early protein//
 25 CONSTANTS family zinc finger//B-box zinc finger//SPRY domain
 TESTI20092170//ENV polyprotein (coat polyprotein)
 TESTI20095200//7TM chemoreceptor
 TESTI20095770//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 30 TESTI20095880//Domain of unknown function DUF33//Penicillin amidase//Formate/nitrite transporter//Sodium:galactoside symporter family TESTI20099350//GGL domain//Clusterin//Biopterin-dependent aromatic amino acid hydroxylase
 TESTI20100090//Lectin C-type domain
 TESTI20104090//TEA domain
 35 TESTI20105910//Notch (DSL) domain//Amiloride-sensitive sodium channel
 TESTI20106170//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 TESTI20106820//Protein kinase C terminal domain
 TESTI20108060//Ser/Thr protein phosphatase
 40 TESTI20112540//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Chorismate synthase//UvrB/uvrC motif
 TESTI20112860//Eukaryotic protein kinase domain
 TESTI20113940//Divalent cation transporter
 TESTI20114480//Zinc finger, C4 type (two domains)//Zinc finger, C2HC type//SAM domain (Sterile alpha motif)//Sterile
 45 alpha motif (SAM)//Pointed domain
 TESTI20116050//UBX domain
 TESTI20120500//Kelch motif//Kelch motif
 TESTI20120900//DNA gyrase/topoisomerase IV, subunit A
 TESTI20121040//Protein phosphatase 2C//Protein phosphatase 2C
 50 TESTI20122070//ELM2 domain//Myb-like DNA-binding domain
 TESTI20125280//Immunoglobulin domain//Immunoglobulin domain
 TESTI20125920//PCI domain
 TESTI20126280//recA bacterial DNA recombination proteins
 TESTI20131440//Carboxypeptidase activation peptide//Zinc carboxypeptidase
 55 TESTI20132310//Ubiquitin carboxyl-terminal hydrolase family 2
 TESTI20134680//MYND finger//B-box zinc finger//CONSTANS family zinc finger//Putative zinc finger in N-recognin
 TESTI20134970//Double-stranded RNA binding motif//Aldehyde oxidase and xanthine dehydrogenase, C terminus//Adenosine-deaminase (editase) domain

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TESTI20140970//Immunoglobulin domain
 TESTI20145780//Src homology domain 2
 TESTI20148380//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//PPR repeat//
 Neuraminidases//ATP synthase Alpha chain, C terminal//TPR Domain//TPR Domain//TPR Domain//TPR Domain//PPR
 5 repeat//TPR Domain
 TESTI20150420//RhoGAP domain
 TESTI20150920//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine
 Rich Repeat
 TESTI20153310//Intermediate filament tail domain
 10 TESTI20162780//Divalent cation transporter
 TESTI20162980//Ubiquitin family//Retroviral aspartyl protease//Retroviral aspartyl protease
 TESTI20164210//Isocitrate and isopropylmalate dehydrogenases//Ribosomal protein S27a//TILa domain//von Wille-
 brand factor type C domain
 TESTI20165990//Ribosomal protein L36
 15 TESTI20166290//Zinc finger, C2H2 type//FAD binding domain//Phosphoenolpyruvate carboxykinase//Ribosomal pro-
 tein S11
 TESTI20166670//Zinc finger C-x8-C-x5-C-x3-H type (and similar).
 TESTI20169500//GGL domain
 TESTI20170280//Flagellar L-ring protein
 20 TESTI20173960//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type
 TESTI20179230//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
 TESTI20182760//Amiloride-sensitive sodium channel
 25 TESTI20183680//Gas vesicles protein GVPc repeated domain
 TESTI20184750//Laminin G domain//Thrombospondin N-terminal -like domains//Laminin G domain
 TESTI20184760//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Transcription
 factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 TESTI20186110//Divalent cation transporter//Translation initiation factor IF-3//Divalent cation transporter
 30 TESTI20193080//Growth-Arrest-Specific Protein 2 Domain
 TESTI20194880//SAP domain
 TESTI20196690//Glycine cleavage T-protein (aminomethyl transferase)
 TESTI20197030//Pancreatic hormone peptides
 TESTI20197600//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 35 TESTI20199110//Disintegrin
 TESTI20205100//DNA gyrase/topoisomerase IV, subunit A
 TESTI20205250//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif//MORN motif
 TESTI20207170//Nucleosome assembly protein (NAP)
 TESTI20210570//CRAL/TRIO domain.
 40 TESTI20212970//DEAD/DEAH box helicase//Helicases conserved C-terminal domain
 TESTI20219110//Eukaryotic protein kinase domain
 TESTI20222030//Hemagglutinin//ATP synthase Alpha chain, C terminal//AMP-binding enzyme
 TESTI20222460//Intermediate filament proteins
 TESTI20227380//DEAD/DEAH box helicase//Helicases conserved C-terminal domain
 45 TESTI20228120//RhoGAP domain
 TESTI20228740//Zinc finger, C2H2 type
 TESTI20244220//Cecropin family//Fes/CIP4 homology domain//Hr1 repeat motif//SH3 domain
 TESTI20244430//Ank repeat//Ank repeat//Ank repeat//SAM domain (Sterile alpha motif)
 TESTI20244460//pKID domain//Adenylate kinase//Thymidylate kinase//ATPases associated with various cellular ac-
 50 tivities (AAA)
 TESTI20246480//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 TESTI20251610//Chitin synthase//von Willebrand factor type A domain
 TESTI20252690//Domain found in Dishevelled, Egl-10, and Pleckstrin
 TESTI20254030//LIM domain containing proteins//LIM domain containing proteins//Villin headpiece domain
 55 TESTI20254990//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 TESTI20255460//ZAP domain//Piwi domain
 TESTI20257910//Class I Histocompatibility antigen, domains alpha 1 and 2//Immunoglobulin domain
 TESTI20258720//Ank repeat//Ank repeat//Ank repeat

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- TESTI202591101/Zinc finger, C3HC4 type (RING finger)//PHD-finger
 TESTI20261040/DNA polymerase (viral) C-terminal domain
 TESTI20261160//PH domain
 TESTI20261680//Hsp20/alpha crystallin family//Granulins
 5 TESTI20262150//Ion transport protein
 TESTI20262940//Phosphofructokinase
 TESTI20264530//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//C.elegans integral membrane protein Srb//WD domain, G-beta repeat//WD domain, G-beta repeat//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain
 10 TESTI20264910//Uteroglobin family
 TESTI20266050//Zinc finger, C3HC4 type (RING finger)//SPRY domain
 TESTI20274960//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 15 TESTI20278280//PMP-22/EMP/MP20/Claudin family
 TESTI20282530//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 TESTI20284260//Histone-like transcription factor (CBF/NF-Y) and archaeal histone//Core histone H2A/H2B/H3/H4
 TESTI20285230//Adenosine-deaminase (editase) domain
 20 THYMU10004280//NHL repeat//NHL repeat
 THYMU20006020//Isocitrate and isopropylmalate dehydrogenases
 THYMU20009500//TPR Domain
 THYMU20013250//LIM domain containing proteins//RI01/ZK632.3/MJ0444 family//Eukaryotic protein kinase domain
 THYMU20018250//TPR Domain
 25 THYMU20019260//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 THYMU20021090//SAM domain (Sterile alpha motif)//Sterile alpha motif (SAM)/Pointed domain
 THYMU20028150//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
 THYMU20028410//BRCA1 C Terminus (BRCT) domain//BRCA1 C Terminus (BRCT) domain
 30 THYMU20031330//4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family
 THYMU20032820//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 THYMU20039320//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 35 THYMU20046350//Cytochrome C and Quinol oxidase polypeptide I
 THYMU20049060//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 THYMU20052830//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
 THYMU20055450//Zona pellucida-like domain
 40 THYMU20055460//Putative esterase
 THYMU20055760//Na+/K+ ATPase C-terminus//Phospholipase A2
 THYMU20062770//Zona pellucida-like domain
 THYMU20063650//Ribulose-phosphate 3 epimerase family//Indole-3-glycerol phosphate synthases
 THYMU20066660//DEAD/DEAH box helicase
 45 THYMU20070250//Transketolase//Dehydrogenase E1 component//Transketolase
 THYMU20071120//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 50 THYMU20077250//HMG (high mobility group) box
 THYMU20081110//LIM domain containing proteins
 THYMU20083390//11S plant seed storage protein
 THYMU20090230//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 THYMU20095920//Iron hydrogenase small subunit
 55 THYMU20097920//PH domain//FERM domain (Band 4.1 family)
 THYMU20098350//bZIP transcription factor//bZIP transcription factor//Tubulin/FtsZ family//Intermediate filament proteins
 THYMU20099060//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain

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- main//Immunoglobulin domain
 THYMU20100940//Protein of unknown function DUF132
 THYMU20104480//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 THYMU20106990//PH domain
- 5 THYMU20110720//Aminotransferases class-III pyridoxal-phosphate
 THYMU20112590//Acyl-CoA dehydrogenase//Adaptin N terminal region
 THYMU20120240//Ubiquitin carboxyl-terminal hydrolases family 2//Ubiquitin carboxyl-terminal hydrolase family 2
 THYMU20120730//Aldehyde dehydrogenase family
 THYMU20121040//bZIP transcription factor//EF-1 guanine nucleotide exchange domain
- 10 THYMU20139160//Uncharacterized protein family UPF0031
 THYMU20143230//EGF-like domain//Extracellular link domain//Fasciclin domain
 THYMU20145990//SH3 domain
 THYMU20153210//7 transmembrane receptor (Secretin family)
 THYMU20170230//Glycine cleavage T-protein (aminomethyl transferase)
- 15 THYMU20176010//WD domain, G-beta repeat//PQQ enzyme repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 THYMU20178440//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
- 20 THYMU20184550//HSF-type DNA-binding domain//bZIP transcription factor
 THYMU20191970//Cadherin domain//Cadherin domain//Cadherin domain//Cadherin domain
 TKIDN10000620//Thioredoxin
 TKIDN10001920//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
- 25 TRACH20011010//5'-nucleotidase
 TRACH20021380//Copper/zinc superoxide dismutase (SODC)//Adenylate and Guanylate cyclase catalytic domain//Adenylate and Guanylate cyclase catalytic domain
 TRACH20029880//MORN motif//MORN motif//Penicillin amidase//Bacterial regulatory proteins, lacI family//Vacuolar sorting protein 9 (VPS9) domain
- 30 TRACH20040390//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)
- 35 //Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)
 TRACH20043360//Kinesin motor domain//Caspase recruitment domain//Ribosomal protein L35
 TRACH20058000//Fibronectin type III domain
 TRACH20090060//C2 domain
 TRACH20091070//Aldehyde dehydrogenase family
- 40 TRACH20093400//Adaptin N terminal region
 TRACH20098510//Ribosomal L29 protein
 TRACH20104510//Uncharacterized protein family UPF0005
 TRACH20108240//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- 45 TRACH20113020//AIR synthase related protein
 TRACH20122980//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain
 TRACH20131230//PH domain//Oxysterol-binding protein
 TRACH20139280//PX domain
 TRACH20143710//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
- 50 TRACH20149500//Zinc finger//Plexin repeat//Cysteine rich repeat//Intermediate filament proteins
 TRACH20149740//Sodium:dicarboxylate symporter family
 TRACH20163470//Putative integral membrane protein DUF46//Sugar (and other) transporter//Sodium:galactoside symporter family
 TRACH20164100//Retroviral aspartyl protease
- 55 TRACH20164810//D-isomer specific 2-hydroxyacid dehydrogenases
 TRACH20167090//Chitinases, family 2
 TRACH20170860//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain

- TRACH20188350//Tropomyosins
 TRACH20190460//Lipase (class 3)
 UTERU20000950//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 5 UTERU20016580//Zinc finger present in dystrophin, CBP/p300//Myb-like DNA-binding domain
 UTERU20026620//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 UTERU20041630//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 10 UTERU20083020//Domain of unknown function DUF71
 UTERU20086530//Lipocalin / cytosolic fatty-acid binding protein family
 UTERU20087070//Sushi domain (SCR repeat)//Trypsin
 UTERU20089390//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain
 15 UTERU20089620//Fringe-like
 UTERU20099040//Cation efflux family
 UTERU20099510//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type
 20 UTERU20104310//RNA polymerases K / 14 to 18 kDa subunit
 UTERU20121140//Rhodanese-like domain
 UTERU20122520//FERM domain (Band 4.1 family)//FERM domain (Band 4.1 family)
 UTERU20127030//Xylose isomerase//ApeE family
 UTERU20127150//Translation initiation factor IF-3//Divalent cation transporter
 25 UTERU20128560//Domain of unknown function DUF28
 UTERU20132620//HMG14 and HMG17
 UTERU20139760//Mitochondrial carrier proteins//Mitochondrial carrier proteins
 UTERU20168960//PH domain//Methanol dehydrogenase beta subunit
 UTERU20181270//Zinc knuckle
 30 UTERU20185220//Bromodomain

EXAMPLE 6

Functional categorization based on the full-length nucleotide sequences

- 35 **[0224]** The functional prediction and categorization of the proteins encoded by the clones were carried out based on the result of homology search of the databases of GenBank, Swiss-Prot, UniGene and nr (see the Homology Search Result Data) for the full-length nucleotide sequences and the result of domain search of the amino acid sequences deduced from the full-length nucleotide sequences (see Example 5).
- 40 **[0225]** The clone predicted to belong to the category of secretory protein/membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extra-cellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it is a secretory or membrane protein, or means a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane domain was suggested by the results of PSORT and SOSUI analyses for deduced ORF.
- 45 **[0226]** The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.
- [0227]** The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.
- 50 **[0228]** The clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes a transcription-related protein.
- 55 **[0229]** The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or means a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, or UniGene, where the hit data corresponds to genes or proteins which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is the human gene and disease database.

[0230] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0231] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0232] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubules, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0233] The clone which is predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0234] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0235] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0236] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0237] The clone predicted to belong to the category of DNA-binding and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0238] The clone predicted to belong to the category of ATP-binding and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0239] In this functional categorization, when a single clone corresponded to multiple categories of those shown above, the clone was assigned to the multiple categories. However, the function of a protein is not restricted to the functional category in this classification, and there is the possibility that other functions are newly assigned to the protein.

[0240] The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 516 clones.

ADRGL20020290, ADRGL20021910, ADRGL20036380, ADRGL20036840, ADRGL20059610, ADRGL20063770, ADRGL20066770, ASTRO20010010, ASTRO20020240, ASTRO20045840, ASTRO20053430, ASTRO20055530, ASTRO20055570, ASTRO20055930, ASTRO20088950, ASTRO20091180, BNGH420021680, BNGH420023870, BNGH420046790, BNGH420052350, BNGH420059680, BNGH420075940, BNGH420077980, BRACE10000510, BRACE20051930, BRACE20052530, BRACE20054080, BRACE20066360, BRACE20068710, BRACE20069000, BRACE20069110, BRACE20194670, BRACE20204670, BRACE20216950, BRAMY10001730, BRAMY20003880, BRAMY20013670, BRAMY20024790, BRAMY20027390, BRAMY20028530, BRAMY20035380, BRAMY20044920, BRAMY20045210, BRAMY20047560, BRAMY20050940, BRAMY20053910, BRAMY20055760, BRAMY20072440, BRAMY20083820, BRAMY20089770, BRAMY20091230, BRAMY20094890, BRAMY20096930, BRAMY20118410, BRAMY20123400, BRAMY20125550, BRAMY20127310, BRAMY20127760, BRAMY20135720, BRAMY20137360, BRAMY20139440, BRAMY20152510, BRAMY20194680, BRAMY20204270, BRAMY20225320, BRAMY20237190, BRAMY20245140, BRAMY20251750, BRAMY20285650, BRAWH20020470, BRAWH20021910, BRAWH20026010, BRAWH20030000, BRAWH20039640, BRAWH20055330, BRAWH20078620, BRAWH20093070, BRAWH20185270, BRCAN10000760, BRCAN10001680, BRCAN20001480, BRCAN20004180, BRCAN20005230, BRCOC20000470, BRCOC20003600, BRHIP10000720, BRHIP10001040, BRHIP20000210, BRSSN20001970, BRSSN20074640, BRSSN20091190, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20041260, CTONG20044870, CTONG20045500, CTONG20049480, CTONG20051450, CTONG20055850, CTONG20056150, CTONG20059130, CTONG20060040, CTONG20063770, CTONG20065680, CTONG20068360, CTONG20069320, CTONG20071680, CTONG20076810, CTONG20078340, CTONG20079590, CTONG20083980, CTONG20084020, CTONG20085210, CTONG20167750, CTONG20168240, CTONG20179890, CTONG20183830, CTONG20184830, DFNES20018000, DFNES20029660, DFNES20057660, DFNES20072990, DFNES20080880, FCBBF20018680, FCBBF20029280, FCBBF20032930, FCBBF20036360, FCBBF20054390, FCBBF30004340, FCBBF30022680, FCBBF30029250, FCBBF30042610, FCBBF30062490, FCBBF30075970, FCBBF30078600, FCBBF30091520, FCBBF30095410, FCBBF30105440, FCBBF30118670, FCBBF30132660, FCBBF30135890, FCBBF30145670, FCBBF30164510, FCBBF30169870, FCBBF30171230, FCBBF30172330, FCBBF30177290, FCBBF30179740, FCBBF30195690, FCBBF30197840, FCBBF30212210, FCBBF30223110, FCBBF30223210, FCBBF30225930, FCBBF30230610,

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FCBBF30260480, FCBBF30266510, FCBBF30287940, FCBBF50000610, FCBBF50004950, FEBRA2000782.0,
FEBRA20018670, FEBRA20031280, FEBRA20031810, FEBRA20038220, FEBRA20039260, FEBRA20040230,
FEBRA20040560, FEBRA20046280, FEBRA20080860, FEBRA20084750, FEBRA20088810, FEBRA20115930,
FEBRA20116650, FEBRA20121950, FEBRA20141980, FEBRA20177800, FEBRA20182030, FEBRA20191720,
5 HCHON10001660, HCHON20015050, HEART10001490, HEART20031680, HHDP10001140, HHDP20051850,
HHDP20082790, HHDP20088160, HLUNG20015070, HLUNG20015180, HLUNG20020850, HLUNG20029490,
HLUNG20032460, HLUNG20033350, HLUNG20034970, HLUNG20037160, HLUNG20041540, HLUNG20042730,
HLUNG20050760, HLUNG20052300, HLUNG20060670, HLUNG20065990, HLUNG20074330, HLUNG20081390,
HLUNG20088750, HLUNG20092530, KIDNE20016360, KIDNE20083150, KIDNE20084030, KIDNE20084040,
10 KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20094670, KIDNE20134130, KIDNE20142900,
KIDNE20143200, KIDNE20148080, KIDNE20160960, KIDNE20163710, KIDNE20169180, KIDNE20182540,
KIDNE20186170, KIDNE20188630, KIDNE20189960, LIVER20007750, LIVER20010510, LIVER20010990,
LIVER20026440, LIVER20030650, LIVER20038000, MESAN20007110, MESAN20008150, MESAN20021220,
MESAN20027900, MESAN20058110, MESAN20059570, MESAN20060430, MESAN20067430, MESAN20084150,
15 MESAN20095220, NT2NE20018740, NT2NE20021860, NT2NE20039210, NT2NE20053230, NT2NE20059210,
NT2NE20064780, NT2NE20069580, NT2NE20080770, NT2NE20082130, NT2NE20092950, NT2NE20140130,
NT2NE20145250, NT2NE20146510, NT2NE20152620, NT2NE20167660, NT2NE20181800, NT2RI20016240,
NT2RI20021200, NT2RI20033920, NT2RP70003110, NT2RP70027790, NT2RP70031070, NT2RP70031480,
NT2RP70056690, NT2RP70087140, NTONG20034540, NTONG20053630, OCBBF20000740, OCBBF20012520,
20 OCBBF20109780, OCBBF20110210, OCBBF20110730, OCBBF20112280, OCBBF20118720, OCBBF20120010,
OCBBF20123200, OCBBF20155030, OCBBF20155900, OCBBF20165910, OCBBF20170350, OCBBF20176650,
OCBBF20185630, OCBBF20191950, PANC10000860, PEBLM20001800, PLACE50001290, PLACE60004260,
PLACE60006300, PLACE60053280, PLACE60055590, PLACE60056910, PLACE60057860, PLACE60061370,
PLACE60064740, PLACE60070500, PLACE60087680, PLACE60104630, PLACE60107010, PLACE60113340,
25 PLACE60138840, PLACE60154450, PLACE60184870, PROST10001100, PROST20011160, PROST20014150,
PROST20035830, PROST20045700, PROST20050390, PROST20065100, PROST20073280, PROST20082430,
PROST20084680, PROST20084720, PROST20099090, PROST20105450, PROST20206060, PROST20108850,
PROST20110120, PROST20114100, PROST20146590, PROST20152510, PROST20168600, PUAEN10000870,
SKMUS20006790, SKMUS20020770, SKMUS20073150, SKMUS20091900, SKNMC20006350, SKNSH20094350,
30 SMINT20006090, SMINT20008110, SMINT20024140, SMINT20028840, SMINT20045470, SMINT20077960,
SMINT20081330, SMINT20086250, SMINT20088440, SMINT20088690, SMINT20092160, SPLEN20015100,
SPLEN20017610, SPLEN20017810, SPLEN20024190, SPLEN20024620, SPLEN20054500, SPLEN20058180,
SPLEN20063890, SPLEN20073880, SPLEN20080070, SPLEN20090880, SPLEN20101950, SPLEN20104690,
SPLEN20105100, SPLEN20108000, SPLEN20110180, SPLEN20110860, SPLEN20118050, SPLEN20121790,
35 SPLEN20125230, SPLEN20136700, SPLEN20138600, SPLEN20139100, SPLEN20175920, SPLEN20177400,
SPLEN20182850, SPLEN20183020, SPLEN20183950, SPLEN20190080, SPLEN20190770, SPLEN20193230,
SPLEN20193490, SPLEN20193790, SPLEN20201830, SPLEN20204670, TESOP10000350, TESTI10000190,
TESTI20006160, TESTI20029100, TESTI20031310, TESTI20032770, TESTI20038240, TESTI20043130,
TESTI20043220, TESTI20045390, TESTI20046540, TESTI20046870, TESTI20047370, TESTI20050400,
40 TESTI20051200, TESTI20051730, TESTI20053260, TESTI20053780, TESTI20057200, TESTI20057590,
TESTI20059080, TESTI20061200, TESTI20062120, TESTI20063330, TESTI20063410, TESTI20063600,
TESTI20066330, TESTI20068530, TESTI20070400, TESTI20070740, TESTI20073460, TESTI20086840,
TESTI20095200, TESTI20095440, TESTI20095880, TESTI20100090, TESTI20102390, TESTI20105910,
TESTI20113940, TESTI20116120, TESTI20121040, TESTI20121710, TESTI20131440, TESTI20142540,
45 TESTI20149880, TESTI20151800, TESTI20162780, TESTI20170170, TESTI20173050, TESTI20182760,
TESTI20183680, TESTI20184750, TESTI20186110, TESTI20198540, TESTI20199110, TESTI20202830,
TESTI20204260, TESTI20210030, TESTI20214630, TESTI20219110, TESTI20244730, TESTI20245600,
TESTI20245860, TESTI20246410, TESTI20251610, TESTI20257910, TESTI20260640, TESTI20261040,
TESTI20262150, TESTI20262940, TESTI20264910, TESTI20271790, TESTI20278280, TESTI20282420,
50 TESTI20282900, TESTI20286590, THYMU20007020, THYMU20012020, THYMU20017270, THYMU20020800,
THYMU20025480, THYMU20028150, THYMU20030690, THYMU20034790, THYMU20046350, THYMU20046770,
THYMU20050010, THYMU20052830, THYMU20054800, THYMU20055740, THYMU20055760, THYMU20062770,
THYMU20078240, THYMU20079690, THYMU20083390, THYMU20087270, THYMU20100940, THYMU20115380,
THYMU20137050, THYMU20137570, THYMU20143230, THYMU20150190, THYMU20153210, THYMU20154790,
55 THYMU20163600, THYMU20171580, THYMU20178440, THYMU20185470, TRACH20011010, TRACH20011540,
TRACH20021380, TRACH20073990, TRACH20081270, TRACH20090060, TRACH20149720, TRACH20149740,
TRACH20159390, TRACH20163470, TRACH20165330, TRACH20167090, TRACH20173680, TRACH20190460,
UMVEN10001380, UTERU20035770, UTERU20040150, UTERU20045200, UTERU20064120, UTERU20086530,

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UTERU20087070, UTERU20087850, UTERU20089300, UTERU20089620, UTERU20095100, UTERU20099040, UTERU20103200, UTERU20125810, UTERU20127030, UTERU20127150, UTERU20139760, UTERU20188840

[0241] The clones predicted to belong to the category of glycoprotein-related protein are the following 121 clones.

ADRGL20020290, ADRGL20036840, ADRGL20059610, ADRGL20066770, ASTRO20055570, BNGH420046790, BNGH420077980, BRACE20051930, BRACE20069000, BRACE20204670, BRACE20216950, BRAMY20013670, BRAMY20089770, BRAMY20251210, BRAWH20039640, BRCAN10000760, BRCAN20005230, BRCOC20003600, CD34C20001750, CTONG20017490, CTONG20036990, CTONG20045500, CTONG20059130, CTONG20079590, CTONG20085210, CTONG20184830, DFNES20018000, DFNES20080880, FCBBF30004340, FCBBF30029250, FCBBF30062490, FCBBF30091520, FCBBF30164510, FCBBF30171230, FCBBF30195690, FCBBF30223210, FEBRA20038220, HCHON20015050, HLUNG20015070, HLUNG20032460, HLUNG20037160, HLUNG20041540, KIDNE20142900, KIDNE20169180, KIDNE20186170, KIDNE20189960, MESAN20021220, MESAN20058110, NT2NE20064780, NT2NE20140130, NT2NE20155650, NT2RP70056690, NTONG20053630, OCBBF20000740, OCBBF20012520, OCBBF20110210, OCBBF20120010, OCBBF20165900, OCBBF20165910, OCBBF20191950, PEBLM20001800, PLACE600004260, PLACE60087680, PLACE60113340, PLACE60184870, PROST20033240, PROST20099090, PROST20108850, PROST20146590, SKMUS20073150, SKNMC20006350, SMINT20028840, SMINT20056230, SMINT20083290, SMINT20091190, SPLEN20024620, SPLEN20063890, SPLEN20080070, SPLEN20090880, SPLEN20118050, SPLEN20139100, SPLEN20183020, SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20043990, TESTI20045390, TESTI20051200, TESTI20057590, TESTI20059080, TESTI20066330, TESTI20086840, TESTI20100090, TESTI20105910, TESTI20154370, TESTI20164210, TESTI20182760, TESTI20184750, TESTI20199110, TESTI20220230, TESTI20245600, TESTI20251610, TESTI20257910, TESTI20286590, THYMU20024500, THYMU20028150, THYMU20052830, THYMU20062770, THYMU20099060, THYMU20170080, THYMU20178440, TRACH20011010, TRACH20011540, TRACH20021380, TRACH20149740, TRACH20170860, TRACH20190460, UTERU20086530, UTERU20087070, UTERU20127030

[0242] The clones predicted to belong to the category of signal transduction-related protein are the following 88 clones.

ASTRO20050810, ASTRO20052420, ASTRO20085080, ASTRO20090680, BNGH420008150, BNGH420015760, BNGH420035290, BNGH420086030, BRAMY20035830, BRAMY20043630, BRAMY20118490, BRAMY20206340, BRAMY20244490, BRAMY20251210, BRAMY20263000, BRAWH20093040, BRAWH20190550, CTONG20004520, CTONG20029030, CTONG20030280, CTONG20063930, CTONG20070720, CTONG20189000, FCBBF30076310, FCBBF30100080, FCBBF30143550, FCBBF30153170, FCBBF30175350, FCBBF30250980, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, HLUNG20084790, KIDNE20089870, KIDNE20160360, LIVER20011640, MESAN20021130, MESAN20027240, MESAN20065990, NT2NE20018890, NT2NE20042550, NT2RP70075800, NTONG20043080, NTONG20048440, PLACE60071800, PROST20033240, PROST20052850, PROST20065790, PROST20075280, SKNSH20052400, SKNSH20057920, SMINT20006020, SMINT20035050, SPLEN20023540, SPLEN20039180, SPLEN20048800, SPLEN20049840, SPLEN20054160, SPLEN20085910, SPLEN20191020, SPLEN20198390, TESTI20046490, TESTI20049060, TESTI20053070, TESTI20066650, TESTI20081890, TESTI20095770, TESTI20106820, TESTI20112860, TESTI20145780, TESTI20150420, TESTI20168880, TESTI20205250, TESTI20228120, TESTI20244220, TESTI20244460, TESTI20251740, TESTI20261160, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20106990, THYMU20145990, THYMU20170080, THYMU20176010, TRACH20188350

[0243] The clones predicted to belong to the category of transcription-related protein are the following 143 clones.

ASTRO20038400, ASTRO20075150, BNGH420070370, BNGH420074600, BNGH420087430, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAWH20040680, BRAWH20050740, BRAWH20080580, BRAWH20082920, BRAWH20095900, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20084660, CTONG20186370, CTONG20186520, DFNES20028170, DFNES20046840, DFNES20073320, FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30093170, FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30143550, FCBBF30220050, FCBBF30228940, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20170240, HCHON10000150, HCHON20002650, HEART20019310, HLUNG20014590, HLUNG20028110, HLUNG20063700, KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20038520, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20061030, NT2NE20079670, NT2NE20082600, NT2RP70001120, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450, OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM20003260, PLACE60052940, PLACE60066970, PLACE60122970, PLACE60150510, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20127450, PROST20151370, PROST20155370, PUAEN10000650, PUAEN20003120, SMINT20011950, SMINT20026200, SMINT20030740, SMINT20039050, SMINT20044140,

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SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20098030, SPLEN20197930, TESTI10001570, TESTI20057430, TESTI20057840, TESTI20059810, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20122070, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20194880, 5 TESTI20197600, TESTI20228740, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20274960, TESTI20282530, THYMU10004280, THYMU20019260, THYMU20032820, THYMU20071120, THYMU20077250, TKIDN10001920, UTERU20016580, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20185220, UTERU20188670

[0244] The clones predicted to belong to the category of disease-related protein are the following 331 clones.

10 ADRGL20020290, ADRGL20021910, ADRGL20026790, ADRGL20036840, ADRGL20059610, ADRGL20066770, ASTRO20038400, ASTRO20052420, ASTRO20055570, ASTRO20075150, ASTRO20088950, BNGH420008150, BNGH420086030, BRACE10000510, BRACE20003310, BRACE20069000, BRACE20097540, BRACE20194670, BRACE20196180, BRACE20204670, BRACE20216950, BRAMY20003540, BRAMY20005080, BRAMY20035830, BRAMY20040580, BRAMY20043630, BRAMY20044920, BRAMY20051820, BRAMY20056620, BRAMY20089770, 15 BRAMY20111780, BRAMY20152510, BRAMY20190550, BRAMY20221600, BRAMY20227860, BRAMY20274510, BRAWH20082920, BRAWH20093040, BRAWH20095900, BRAWH20190530, BRAWH20191980, BRCAN10000760, BRCAN10001050, BRCAN20005230, BRSSN20066440, CTONG20004520, CTONG20029030, CTONG20042640, CTONG20045500, CTONG20052780, CTONG20053990, CTONG20070780, CTONG20070910, CTONG20072930, CTONG20083980, CTONG20084660, CTONG20165750, CTONG20169040, CTONG20183430, CTONG20183830, 20 CTONG20186290, CTONG20189000, DFNES20016470, DFNES20025500, DFNES20046840, DFNES20055400, DFNES20080880, FCBBF10000230, FCBBF20035490, FCBBF20066340, FCBBF30002270, FCBBF30002280, FCBBF30019140, FCBBF30053300, FCBBF30071500, FCBBF30072440, FCBBF30076310, FCBBF30080730, FCBBF30100080, FCBBF30115920, FCBBF30118670, FCBBF30129010, FCBBF30132050, FCBBF30136230, FCBBF30153170, FCBBF30164510, FCBBF30166220, FCBBF30171230, FCBBF30175350, FCBBF30194550, 25 FCBBF30220050, FCBBF30223210, FCBBF30259050, FCBBF30263080, FCBBF30275590, FCBBF50001650, FEBRA20027070, FEBRA20045380, FEBRA20046200, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20078800, FEBRA20087550, FEBRA20088810, FEBRA20090160, FEBRA20092760, FEBRA20151750, FEBRA20170240, FEBRA20173330, FEBRA20191720, HCHON10000150, HCHON20015050, HEART20C09590, HEART20022200, HEART20063100, HHDPC20081230, HLUNG20008460, HLUNG20014590, HLUNG20032460, 30 HLUNG20063700, HLUNG20065990, HLUNG20069350, HLUNG20081530, HLUNG20082350, HLUNG20083330, HLUNG20085210, KIDNE20081170, KIDNE20084040, KIDNE20088240, KIDNE20089870, KIDNE20133460, KIDNE20134890, KIDNE20141700, KIDNE20142900, KIDNE20150730, KIDNE20152440, KIDNE20160360, KIDNE20165390, KIDNE20169180, KIDNE20173430, KIDNE20189960, LIVER20026440, MESAN20006200, MESAN20021130, MESAN20033220, MESAN20056890, MESAN20057240, MESAN20065990, MESAN20067430, 35 MESAN20069530, NESOP20004520, NT2NE20018890, NT2NE20026200, NT2NE20037050, NT2NE20053950, NT2NE20061030, NT2NE20111190, NT2NE20117580, NT2NE20119980, NT2NE20140130, NT2NE20141040, NT2RI20093010, NT2RP70003110, NT2RP70046410, NT2RP70075300, NTONG20032100, NTONG20034540, OCBBF20000740, OCBBF20012520, OCBBF20111600, OCBBF20120010, OCBBF20156450, OCBBF20157970, OCBBF20191950, PEBLM20001800, PEBLM20003260, PLACE60004260, PLACE60012620, PLACE60054230, 40 PLACE60054870, PLACE60062660, PLACE60087680, PLACE60184870, PROST20015210, PROST20024250, PROST20036350, PROST20050390, PROST20058860, PROST20063430, PROST20065790, PROST20084720, PROST20099090, PROST20120070, PROST20127450, PROST20146590, PROST20152510, PROST20168600, PUAEN10000650, PUAEN20003120, SKMUS20008730, SKMUS20017400, SKMUS20040440, SKMUS20073590, SKMUS20079150, SKNSH20009710, SMINT20002320, SMINT20007470, SMINT20008110, SMINT20011950, 45 SMINT20016150, SMINT20026200, SMINT20030740, SMINT20049920, SMINT20077960, SMINT20083290, SMINT20086250, SMINT20089600, SMINT20091190, SPLEN20023540, SPLEN20024190, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20057830, SPLEN20059270, SPLEN20063890, SPLEN20073500, SPLEN20080070, SPLEN20085910, SPLEN20090880, SPLEN20098030, SPLEN20118050, SPLEN20136730, SPLEN20138600, SPLEN20139100, SPLEN20139360, SPLEN20180980, SPLEN20187490, SPLEN20193790, 50 SPLEN20201830, TESTI10000190, TESTI20031310, TESTI20035790, TESTI20041630, TESTI20049060, TESTI20050720, TESTI20051200, TESTI20057430, TESTI20057590, TESTI20059080, TESTI20062120, TESTI20067480, TESTI20071630, TESTI20099350, TESTI20105130, TESTI20105910, TESTI20108060, TESTI20125920, TESTI20130530, TESTI20131440, TESTI20134680, TESTI20142540, TESTI20143180, TESTI20150420, TESTI20154370, TESTI20164210, TESTI20166670, TESTI20168880, TESTI20171070, 55 TESTI20182760, TESTI20184750, TESTI20193080, TESTI20194880, TESTI20196970, TESTI20197600, TESTI20201760, TESTI20207170, TESTI20219110, TESTI20228740, TESTI20244430, TESTI20246480, TESTI20251740, TESTI20252690, TESTI20254030, TESTI20257910, TESTI20258720, TESTI20266050, TESTI20271790, TESTI20274960, TESTI20282530, TESTI20286590, THYMU10004280, THYMU20006020,

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THYMU20013250, THYMU20019260, THYMU20023560, THYMU20028150, THYMU20032820, THYMU20034400, THYMU20055460, THYMU20063650, THYMU20070250, THYMU20071120, THYMU20081110, THYMU20090230, THYMU20095920, THYMU20098350, THYMU20099060, THYMU20120730, THYMU20121040, THYMU20170080, THYMU20185650, THYMU20191970, TKIDN10000620, TKIDN10001920, TRACH20011540, TRACH20091070, TRACH20143710, TRACH20170860, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20086530, UTERU20087070, UTERU20087850, UTERU20099510, UTERU20101150, UTERU20104310, UTERU20127030, UTERU20185220

[0245] In particular, hit data of the following 328 clones for Swiss-Prot, or GenBank, UniGene, or nr corresponded to genes or proteins which had been deposited in the Online Mendelian Inheritance in Man (OMIM), which is the human gene and disease database, (the OMIM Number is shown in the parenthesis after the Clone Name).

ADRGL20020290 (602193), ADRGL20021910 (605717), ADRGL20026790 (605046), ADRGL20036840 (142800), ADRGL20059610 (230800;230900;231000;231005), ADRGL20066770 (130660), ASTRO20038400 (604764), ASTRO20052420 (600888), ASTRO20055570 (176640;123400;137440;245300;600072), ASTRO20075150 (601896), ASTRO20088950 (603202;223000;223100), BNGH420008150 (600050), BNGH420086030 (118423), BRACE10000510 (148021), BRACE20003310 (603899), BRACE20069000 (204200), BRACE20097540 (604908), BRACE20194670 (314375), BRACE20196180 (605535), BRACE20204670 (176884), BRACE20216950 (158070), BRAMY20003540 (602142), BRAMY20005080 (604735), BRAMY20035830 (603524), BRAMY20040580 (604077), BRAMY20043630 (602775), BRAMY20044920 (603486), BRAMY20051820 (604567), BRAMY20056620 (210210), BRAMY20089770 (602566), BRAMY20111780 (604077), BRAMY20152510 (176879), BRAMY20190550 (600051), BRAMY20221600 (605789), BRAMY20227860 (605416), BRAMY20274510 (180475), BRAWH20082920 (603246), BRAWH20093040 (602989), BRAWH20095900 (602277), BRAWH20190530 (605208), BRAWH20191980 (239500), BRCAN10000760 (111000), BRCAN10001050 (603696), BRCAN20005230 (603268), BRSSN20066440 (603430), CTONG20004520 (603817), CTONG20029030 (602775), CTONG20042640 (103390), CTONG20045500 (106195), CTONG20052780 (605612), CTONG20053990 (602187), CTONG20070780 (118990), CTONG20070910 (604450), CTONG20072930 (314995), CTONG20083980 (601703), CTONG20084660 (600834), CTONG20165750 (182465), CTONG20169040 (148030), CTONG20183430 (106410), CTONG20183830 (600382), CTONG20186290 (100660), CTONG20189000 (600888), DFNES20016470 (605952), DFNES20025500 (604581), DFNES20046840 (602617;241850), DFNES20055400 (603456), DFNES20080880 (602273), FCBBF10000230 (602327), FCBBF20035490 (602489), FCBBF20066340 (603560), FCBBF30002270 (142708), FCBBF30002280 (176763), FCBBF30019140 (602120), FCBBF30053300 (600299), FCBBF30071500 (125485), FCBBF30072440 (604455), FCBBF30076310 (176892), FCBBF30080730 (600572), FCBBF30100080 (602488), FCBBF30115920 (603577), FCBBF30118670 (603640), FCBBF30129010 (601260), FCBBF30132050 (603018), FCBBF30136230 (189909), FCBBF30153170 (171860;171850), FCBBF30164510 (603006), FCBBF30166220 (182144), FCBBF30171230 (162151), FCBBF30175350 (602521), FCBBF30194550 (182900), FCBBF30220050 (600380), FCBBF30223210 (300022), FCBBF30263080 (194558), FCBBF30275590 (601403), FCBBF50001650 (605268), FEBRA20027070 (314995), FEBRA20045380 (602942), FEBRA20046200 (106410), FEBRA20046510 (604077), FEBRA20057010 (602187), FEBRA20063720 (603899), FEBRA20078800 (601825;256000), FEBRA20087550 (600811), FEBRA20088810 (603725), FEBRA20090160 (600137), FEBRA20092760 (602567), FEBRA20170240 (314997), FEBRA20173330 (602990), FEBRA20191720 (603895), HCHON10000150 (300163), HCHON20015050 (151510), HEART20009590 (604581), HEART20022200 (601870), HEART20063100 (602422), HHDP20081230 (164035), HLUNG20008460 (300108), HLUNG20014590 (604077), HLUNG20032460 (176785), HLUNG20063700 (600210), HLUNG20065990 (186591), HLUNG20069350 (114212), HLUNG20081530 (162230), HLUNG20082350 (604677), HLUNG20083330 (120180), HLUNG20085210 (604464), KIDNE20081170 (604535), KIDNE20084040 (602382), KIDNE20088240 (605084), KIDNE20089870 (602922), KIDNE20133460 (605430), KIDNE20134890 (117143), KIDNE20141700 (312760), KIDNE20142900 (188040), KIDNE20150730 (179715), KIDNE20152440 (602194), KIDNE20160360 (602488), KIDNE20165390 (604649), KIDNE20169180 (191845), KIDNE20173430 (603831), KIDNE20189960 (275360), LIVER20026440 (601270), MESAN20006200 (151740), MESAN20021130 (600050), MESAN20033220 (600466), MESAN20056890 (600813), MESAN20057240 (126380), MESAN20065990 (601959), MESAN20067430 (191010), MESAN20069530 (604362), NESOP20004520 (153432), NT2NE20018890 (606031), NT2NE20026200 (277730), NT2NE20037050 (300028), NT2NE20053950 (604078), NT2NE20061030 (600834), NT2NE20111190 (602619), NT2NE20117580 (601825;256000), NT2NE20119980 (191161), NT2NE20140130 (601281), NT2NE20141040 (602917), NT2RI20093010 (172460), NT2RP70003110 (130160;194050), NT2RP70046410 (601930), NT2RP70075300 (601856), NTONG20032100 (148065;193900), NTONG20034540 (602658), OCBBF20000740 (602059), OCBBF20012520 (602059), OCBBF20111600 (147625), OCBBF20120010 (605008), OCBBF20156450 (314997), OCBBF20157970 (604077), OCBBF20191950 (192977), PEBLM20001800 (146900), PEBLM20003260 (194558), PLACE60004260 (601891), PLACE60012620 (214500), PLACE60054230 (300108), PLACE60054870 (160776),

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PLACE60062660 (606004),
 PLACE60087680 (146732), PLACE60184870 (172425), PROST20015210 (160745), PROST20024250 (604078),
 PROST20036350 (138295), PROST20050390 (601258), PROST20058860 (182282), PROST20063430 (603292),
 PROST20065790 (171840), PROST20084720 (604426), PROST20099090 (602714), PROST20120070 (602809),
 5 PROST20127450 (602960), PROST20146590 (158340;113720), PROST20152510 (603367), PROST20168600
 (604415), PUAEN10000650 (602960), PUAEN20003120 (601573), SKMUS20008730 (602127), SKMUS20017400
 (191030), SKMUS20040440 (604163), SKMUS20073590 (605834), SKMUS20079150 (605596), SKNSH20009710
 (191030;164970), SMINT20002320 (601644), SMINT20007470 (190370), SMINT20008110 (604384),
 SMINT20011950 (603430), SMINT20016150 (134790), SMINT20026200 (159556), SMINT20030740 (604078),
 10 SMINT20049920 (600417), SMINT20077960 (137350;105120), SMINT20083290 (146900), SMINT20086250
 (238330), SMINT20089600 (605926), SMINT20091190 (146900), SPLEN20023540 (605577), SPLEN20024190
 (601548), SPLEN20042200 (604167), SPLEN20043680 (126340;234050;278730), SPLEN20055600 (194541),
 SPLEN20057830 (179715), SPLEN20059270 (602165), SPLEN20063890 (600245), SPLEN20073500 (603300),
 SPLEN20080070 (230000), SPLEN20085910 (603424), SPLEN20090880 (142800), SPLEN20098030 (601742),
 15 SPLEN20118050 (301870), SPLEN20136730 (605412), SPLEN20138600 (603728), SPLEN20139100 (147120),
 SPLEN20139360 (117140), SPLEN20180980 (156560), SPLEN20187490 (179838), SPLEN20193790 (147150),
 SPLEN20201830 (301870), TESTI10000190 (158340;113720),
 TESTI20031310 (107280), TESTI20035790 (601940), TESTI20049060 (603889), TESTI20050720 (245050),
 TESTI20051200 (602273), TESTI20057430 (194532), TESTI20057590 (601890), TESTI20059080 (604038),
 20 TESTI20062120 (604212), TESTI20067480 (602277), TESTI20071630 (602692), TESTI20099350 (160776),
 TESTI20105130 (310400), TESTI20105910 (601328), TESTI20108060 (600590), TESTI20125920 (601934),
 TESTI20130530 (146680), TESTI20131440 (114850), TESTI20134680 (117143), TESTI20142540 (137960),
 TESTI20143180 (117143), TESTI20150420 (602732), TESTI20154370 (600936), TESTI20164210 (602319),
 TESTI20166670 (142968), TESTI20168880 (151410), TESTI20171070 (604064), TESTI20182760 (601328),
 25 TESTI20184750 (150320), TESTI20193080 (602128), TESTI20194880 (602260), TESTI20196970 (601117),
 TESTI20197600 (604167), TESTI20201760 (602162), TESTI20207170 (480100), TESTI20219110 (601890),
 TESTI20228740 (604027), TESTI20244430 (182900), TESTI20246480 (601486), TESTI20251740 (602731),
 TESTI20252690 (601368), TESTI20254030 (602330), TESTI20257910 (142871), TESTI20258720 (182900),
 TESTI20266050 (109092), TESTI20271790 (604678), TESTI20274960 (194558), TESTI20282530 (604077),
 30 TESTI20286590 (147267), THYMU10004280 (602290), THYMU20006020 (601149), THYMU20013250 (601988),
 THYMU20019260 (603899), THYMU20023560 (142765), THYMU20028150 (190197), THYMU20032820 (604077),
 THYMU20034400 (604449), THYMU20055460 (133280), THYMU20063650 (180480), THYMU20070250 (277730),
 THYMU20071120 (603899), THYMU20081110 (602567), THYMU20090230 (602324), THYMU20095920 (605349),
 THYMU20098350 (148040;131760;131800;131900), THYMU20099060 (146900), THYMU20120730 (100660),
 35 THYMU20121040 (130592), THYMU20170080 (604964), THYMU20185650 (602121;124900), THYMU20191970
 (604265), TKIDN10000620 (605072), TKIDN10001920 (603899), TRACH20011540 (191155), TRACH20091070
 (100660), TRACH20143710 (601905), TRACH20170860 (147170), UTERU10001060 (311040), UTERU20026620
 (314997), UTERU20041630 (602277),
 UTERU20086530 (173310), UTERU20087070 (216950), UTERU20087850 (605248), UTERU20099510 (604077),
 40 UTERU20101150 (164012), UTERU20104310 (604414), UTERU20127030 (150325), UTERU20185220 (600014)
[0246] The clones predicted to belong to the category of enzyme and/or metabolism-related protein are the following
 219 clones.
 ADRGL20059610, ASTRO20026320, ASTRO20050810, ASTRO20088950, BNGH420008150, BNGH420035290,
 BNGH420074600, BRACE20050870, BRACE20097540, BRACE20200770, BRACE20204670, BRACE20215410,
 45 BRAMY20003540, BRAMY20005080, BRAMY20027990, BRAMY20028620, BRAMY20044920, BRAMY20055760,
 BRAMY20056620, BRAMY20072870, BRAMY20093490, BRAMY20096930, BRAMY20118490, BRAMY20125360,
 BRAMY20143870, BRAMY20152510, BRAMY20231150, BRAMY20244490, BRAMY20251210, BRAWH20021910,
 BRAWH20082920, BRAWH20093040, BRAWH20094900, BRAWH20183170, BRAWH20188750, BRAWH20190550,
 BRAWH20191980, BRCAN20005230, BRCOC20003600, CTONG20051100, CTONG20070910, CTONG20076810,
 50 CTONG20079590, CTONG20080140, CTONG20085210, CTONG20186290, DFNES20063460, DFNES20080880,
 FCBBF20023490, FCBBF20066340, FCBBF30004340, FCBBF30019140, FCBBF30022680, FCBBF30029250,
 FCBBF30072440, FCBBF30076310, FCBBF30085560, FCBBF30091520, FCBBF30107290, FCBBF30125880,
 FCBBF30132050, FCBBF30143550, FCBBF30153170, FCBBF30166220, FCBBF30171230, FCBBF30175350,
 FCBBF30236670, FCBBF30260480, FEBRA20038220, FEBRA20040560, FEBRA20078800, FEBRA20090160,
 55 FEBRA20172230, FEBRA20173330, HCHON20000870, HCHON20002710, HEART10001490, HEART20022200,
 HEART20047640, HEART20082570, HLUNG20011260, HLUNG20032460, HLUNG20041540, HLUNG20042730,
 HLUNG20054790, KIDNE20080690, KIDNE20083620, KIDNE20084040, KIDNE20147170, KIDNE20152440,
 KIDNE20173150, KIDNE20186170, KIDNE20189960, LIVER20011640, LIVER20026440, LIVER20055270,

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MESAN20021130, MESAN20033220, MESAN20038520, ME5AN20057240, MESAN20058110, MESAN20065990, MESAN20095800, NT2NE20026200, NT2NE20042550, NT2NE20117580, NT2NE20127900, NT2RI20093010, NT2RP70064570, NTONG20034540, NTONG20043080, NTONG20053630, NTONG20053730, NTONG20058010, OCBBF20120010, OCBBF20167290, OCBBF20191950, PANCRI10000860, PLACE60052940, PLACE60064180, PLACE60073090, PLACE60095600, PLACE60184410, PLACE60188630, PROST20007600, PROST20033240, PROST20036350, PROST20039300, PROST20050390, PROST20051310, PROST20052850, PROST20065790, PROST20075280, PROST20084720, PROST20099090, PROST20108850, PROST20152510, PUAEN20001520, PUAEN20002470, SKNMC20006350, SKNSH20057920, SMINT20008110, SMINT20049920, SMINT20094680, SPLEN20023540, SPLEN20024930, SPLEN20043680, SPLEN20048800, SPLEN20054500, SPLEN20057900, SPLEN20071820, SPLEN20080070, SPLEN20085910, SPLEN20108000, SPLEN20136730, SPLEN20180980, TESTI20012080, TESTI20030200, TESTI20031310, TESTI20038240, TESTI20050720, TESTI20051200, TESTI20059080, TESTI20062120, TESTI20066330, TESTI20076570, TESTI20103690, TESTI20105130, TESTI20106820, TESTI20108060, TESTI20112860, TESTI20121040, TESTI20130530, TESTI20131440, TESTI20168880, TESTI20170170, TESTI20196690, TESTI20196970, TESTI20199110, TESTI20205250, TESTI20212970, TESTI20222030, TESTI20226520, TESTI20227380, TESTI20244460, TESTI20244730, TESTI20250630, TESTI20260640, TESTI20262940, TESTI20264530, TESTI20285230, THYMU20006020, THYMU20013250, THYMU20034400, THYMU20039320, THYMU20055460, THYMU20055760, THYMU20063650, THYMU20066660, THYMU20070250, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20110720, THYMU20120240, THYMU20120730, THYMU20170230, TRACH20011010, TRACH20021380, TRACH20091070, TRACH20113020, TRACH20143710, TRACH20164100, TRACH20190460, UTERU20087070, UTERU20089620, UTERU20104310, UTERU20185220, UTERU20188670

[0247] The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 44 clones.

ASTRO20090680, BRACE20079370, BRAMY20234820, BRCAN10001050, BRCAN20005410, CTONG20032930, FCBBF20070950, FCBBF30002270, FCBBF30053300, FCBBF30105860, FCBBF30175350, FCBBF30215240, FCBBF30275590, FEBRA20045380, HLUNG20068120, KIDNE20134890, KIDNE20150730, MESAN20021470, NT2NE20077250, NT2NE20153620, NT2RP70030840, NTONG20053910, OCBBF20111370, OCBBF20174580, PROST20063430, SKNMC10001230, SMINT20028800, SPLEN20023540, SPLEN20057830, SPLEN20139360, TESTI20031410, TESTI20057840, TESTI20065650, TESTI20066650, TESTI20107320, TESTI20108060, TESTI20114480, TESTI20134680, TESTI20143180, TESTI20150920, TESTI20201760, TESTI20278280, TESTI20284260, THYMU20097920

[0248] The clones predicted to belong to the category of cytoskeleton-related protein are the following 80 clones.

ADRG20062330, ASTRO20053430, BGGI120000670, BRACE20079370, BRAMY20038980, BRAMY20083330, BRAMY20094890, CTONG20004110, CTONG20032930, CTONG20077760, CTONG20083980, CTONG20169040, CTONG20183430, DFNES20018000, FCBBF30105860, FCBBF30130410, FCBBF30194550, FCBBF30201630, FCBBF30271990, FEBRA20005040, FEBRA20046200, FEBRA20099860, HCHON20015050, HLUNG20081530, KIDNE20081170, NT2RP70001730, NT2RP70003110, NTONG20032100, OCBBF20166890, OCBBF20174890, PLACE60054870, PLACE60055590, PLACE60071800, PLACE60118810, PROST20015210, PROST20097840, PROST20120070, PROST20146590, SKMUS20007260, SKMUS20008730, SKMUS20017400, SKMUS20073590, SMINT20062050, SMINT20074330, SMINT20077960, SPLEN20039180, SPLEN20049840, SPLEN20076470, SPLEN20182990, SPLEN20187490, SPLEN20195710, TESTI10000190, TESTI20041630, TESTI20057880, TESTI20058920, TESTI20060080, TESTI20064530, TESTI20064650, TESTI20065650, TESTI20067440, TESTI20071130, TESTI20099350, TESTI20112540, TESTI20125280, TESTI20136010, TESTI20153310, TESTI20175370, TESTI20222460, TESTI20244430, TESTI20254030, TESTI20258720, THYMU20024500, THYMU20062610, THYMU20098350, TRACH20043360, TRACH20098510, TRACH20149500, UTERU20089390, UTERU20122520, UTERU20168960

[0249] The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 70 clones.

ASTRO20026320, BRACE20050870, BRACE20200770, BRAMY20134050, BRAWH20063010, BRAWH20093040, BRAWH20174330, BRAWH20176850, CTONG20042640, FCBBF20023490, FCBBF20035490, FCBBF20070950, FCBBF30002270, FCBBF30048420, FCBBF30080730, FCBBF30115920, FCBBF30236670, FEBRA20035240, FEBRA20092760, FEBRA20173330, HHDPC20081230, HLUNG20011460, HLUNG20068120, KIDNE20089870, KIDNE20150730, MESAN20056890, MESAN20057240, NT2NE20037050, NT2NE20167660, NT2RP70031070, NTONG20053730, PLACE60064180, PLACE60095600, PROST20016760, PROST20051310, PROST20058860, PROST20152510, PUAEN20002470, SKMUS20079150, SKNSH20030640, SPLEN20023850, SPLEN20057830, SPLEN20139360, SPLEN20190430, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20062120, TESTI20065650, TESTI20081890, TESTI20150920, TESTI20153310, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20251740, TESTI20256560, TESTI20260640, TESTI20270130,

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TESTI20284260, TESTI20285230, THYMU20021090, THYMU20049060, THYMU20066660, THYMU20081110, THYMU20090230, THYMU20120240, UTERU10001060, UTERU20104310

[0250] The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 20 clones.

- 5 BRAMY20038980, BRAMY20274510, CTONG20008190, CTONG20033610, FCBBF20018680, FEBRA20090220, KIDNE20141700, NT2NE20167660, NTONG20055200, PLACE60012620, PROST20036350, PROST20062820, SKMUS20040440, SMINT20000070, SPLEN20180980, TESTI20055680, TESTI20067440, TESTI20107240, THYMU20096580, THYMU20121040

[0251] The clones predicted to belong to the category of cellular defense-related protein are the following 10 clones.

10 ASTRO20089600, BRAMY20117670, FEBRA20087550, HLUNG20081390, MESAN20057240, NTONG20031580, PROST20007600, SPLEN20023850, SPLEN20043680, TESTI20261680

[0252] The clones predicted to belong to the category of development and/or differentiation-related protein are the following 19 clones.

- 15 BRACE20061620, BRACE20200770, BRAMY20013670, CTONG20017490, CTONG20020950, HCHON10000150, MESAN20021470, OCBBF20165910, PROST20155370, PUAEN20002470, TESTI20079220, TESTI20079980, TESTI20166670, TESTI20184760, TESTI20252690, TRACH20040390, UTERU20089620, UTERU20094830, UTERU20169020

[0253] The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 168 clones.

- 20 ASTRO20038400, BGGI120010750, BNGH420070370, BRACE20003310, BRACE20061620, BRAMY20001510, BRAMY20040580, BRAMY20076100, BRAMY20111780, BRAMY20274510, BRAWH20040680, BRAWH20050740, BRAWH20063010, BRAWH20080580, BRAWH20095900, BRAWH20174330, BRSSN20066440, CTONG20020950, CTONG20044230, CTONG20053990, CTONG20072930, CTONG20074000, CTONG20165750, CTONG20186370, CTONG20186520, DFNES20046840, DFNES20073320, FCBBF20035430, FCBBF20070950, FCBBF30002270, 25 FCBBF30003610, FCBBF30019140, FCBBF30021900, FCBBF30048420, FCBBF30080730, FCBBF30093170, FCBBF30114850, FCBBF30129010, FCBBF30136230, FCBBF30220050, FCBBF30228940, FCBBF30236670, FCBBF30263080, FCBBF30285930, FCBBF50003530, FEBRA20026820, FEBRA20027070, FEBRA20035240, FEBRA20046510, FEBRA20057010, FEBRA20063720, FEBRA20087550, FEBRA20092760, FEBRA20170240, FEBRA20177800, HCHON20002650, HEART20019310, HEART20063100, HHDP20081230, HLUNG20011460, 30 HLUNG20014590, HLUNG20028110, HLUNG20063700, HLUNG20068120, KIDNE20140870, LIVER20006260, MESAN20016270, MESAN20056890, MESAN20057240, NT2NE20038870, NT2NE20053950, NT2NE20060750, NT2NE20079670, NT2NE20082600, NT2NE20087270, NT2RP70029780, NT2RP70046410, NT2RP70057500, NT2RP70075300, NT2RP70090870, OCBBF20116250, OCBBF20120950, OCBBF20121910, OCBBF20156450, OCBBF20157970, OCBBF20166900, OCBBF20175360, OCBBF20177540, PEBLM10001470, PEBLM20003260, 35 PLACE60066970, PLACE60122970, PLACE60177880, PROST20007170, PROST20024250, PROST20035170, PROST20051310, PROST20058860, PROST20151370, PROST20155370, PUAEN20003120, SMINT20011950, SMINT20030740, SMINT20039050, SMINT20044140, SMINT20086720, SPLEN20042200, SPLEN20043680, SPLEN20055600, SPLEN20059270, SPLEN20063250, SPLEN20139360, SPLEN20190430, TESTI10001570, TESTI20006830, TESTI20030200, TESTI20031410, TESTI20035790, TESTI20057430, TESTI20059810, 40 TESTI20062120, TESTI20067480, TESTI20068790, TESTI20075240, TESTI20079220, TESTI20088840, TESTI20104090, TESTI20134970, TESTI20166670, TESTI20171070, TESTI20173960, TESTI20184760, TESTI20197600, TESTI20201760, TESTI20212970, TESTI20227380, TESTI20228740, TESTI20246480, TESTI20254030, TESTI20254990, TESTI20266050, TESTI20268240, TESTI20270130, TESTI20274960, TESTI20282530, TESTI20284260, TESTI20285230, THYMU10004280, THYMU20019260, THYMU20023560, 45 THYMU20032820, THYMU20049060, THYMU20066660, THYMU20071120, THYMU20077250, THYMU20081110, THYMU20090230, TKIDN10001920, TRACH20108240, UTERU10001060, UTERU20026620, UTERU20041630, UTERU20094830, UTERU20099510, UTERU20101150, UTERU20169020, UTERU20177150, UTERU20188670

[0254] The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 93 clones.

- 50 ASTRO20026320, BNGH420035290, BRACE20050870, BRACE20079370, BRACE20200770, BRAMY20055760, BRAMY20118490, BRAMY20244490, BRAMY20251210, BRAWH20093040, BRAWH20190550, BRCAN10001050, BRCC20003600, CTONG20008190, CTONG20030280, CTONG20032930, CTONG20176040, CTONG20184830, FCBBF20023490, FCBBF30019140, FCBBF30076310, FCBBF30105860, FCBBF30175350, FCBBF30201630, FCBBF30236670, FEBRA20005040, FEBRA20090160, FEBRA20173330, HCHON20000870, HLUNG20011260, 55 HLUNG20052300, KIDNE20081170, KIDNE20134890, LIVER20030650, LIVER20055270, MESAN20065990, NT2NE20042550, NTONG20043080, NTONG20055200, OCBBF20182060, PLACE60054870, PLACE60064180, PLACE60095600, PLACE60140640, PROST20015210, PROST20033240, PROST20036350, PROST20051310, PROST20052850, PROST20062820, PROST20075280, PROST20120070, PUAEN20002470, SKNSH20052400,

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SKNSH20057920, SMINT20008110, SPLEN20023850, SPLEN20043680, SPLEN20049840, SPLEN20136730, SPLEN20180980, SPLEN20193790, TESTI20055680, TESTI20058920, TESTI20060080, TESTI20064650, TESTI20071130, TESTI20099350, TESTI20106820, TESTI20112860, TESTI20134680, TESTI20136010, TESTI20143180, TESTI20175370, TESTI20212970, TESTI20222460, TESTI20227380, TESTI20244220, TESTI20244460, TESTI20264530, THYMU20013250, THYMU20039320, THYMU20062610, THYMU20066660, THYMU20087270, THYMU20096580, THYMU20100940, THYMU20176010, TRACH20043360, TRACH20098510, TRACH20113020, UTERU20185220, UTERU20188670

[0255] Among the clones other than the ones shown above, BNGH420036410 and FCBBF30257370 are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

SMINT20044730, TESTI20140970

[0256] The two clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20055560, CTONG20046690, DFNES20043710, FCBBF30005500, MESAN20030350, MESAN20030370, PLACE60074820, TESTI20058350, TESTI20106170, TRACH20131230, UTERU20000950

[0257] The 11 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

ASTRO20010290, BRACE20099070, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20184550

[0258] The 18 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

ADRGL20047770, ADRGL20079060, BRACE20014450, BRACE20051600, BRAWH20185260, CTONG20033750, CTONG20070090, CTONG20190290, FCBBF20020440, FCBBF30005360, FCBBF30173960, FEBRA20031000, KIDNE20087880, LIVER20013890, MESAN20030350, MESAN20030370, OCBBF20113110, PLACE60074820, PLACE60093380, PROST20028970, PROST20102190, SALGL10001070, SPLEN20006950, SPLEN20011350, SPLEN20050090, TESTI20060830, TESTI20066150, TESTI20120900, TESTI20132310, TESTI20148380, TESTI20162980, TESTI20166290, TESTI20205100, THYMU20112590, TRACH20029880

[0259] The 35 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

PLACE60054820, TESTI20197030

[0260] The two clones shown above are clones which were predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

ASTRO20006530, OCBBF20016390, TRACH20058000

[0261] The three clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

BRACE20065470, PLACE60054820

[0262] The two clones shown above are clones which were predicted to highly possibly belong to the category of nuclear protein and/or RNA synthesis-related protein based on the result of domain search by Pfam.

ASTRO20010290, BRACE20099070, BRAWH20014590, CTONG20007660, DFNES20076340, DFNES20094820, FCBBF30125460, FCBBF30142290, FCBBF30169280, FEBRA20031000, MESAN20034440, NT2NE20026510, NT2RP70031340, PLACE50001390, SPLEN20135030, TESTI20046890, TESTI20060350, TESTI20166290, TESTI20259110, THYMU20104480, THYMU20184550

[0263] The 21 clones shown above are clones which were predicted to highly possibly belong to the category of DNA-binding and/or RNA-binding protein based on the result of domain search by Pfam.

KIDNE20133880, MESAN20030350, MESAN20030370, TESTI20059480

[0264] The four clones shown above are clones which were predicted to highly possibly belong to the category of ATP-binding and/or GTP-binding protein based on the result of domain search by Pfam.

[0265] The 205 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search for their full-length nucleotide sequences and motif search in their deduced ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (/), are shown below.

ADRGL20022600//DIAPHANOUS PROTEIN HOMOLOG 1 (P140MDIA).

ADRGL20023920//ABC1 PROTEIN HOMOLOG PRECURSOR.

ASTRO20001910//Rattus norvegicus mRNA for annexin V-binding protein (ABP-10), partial cds.

ASTRO20009140//PUTATIVE COMPETENCE-DAMAGE PROTEIN.

ASTRO20046280//PSU1 PROTEIN.

ASTRO20058960//DNA damage inducible protein homolog - fission yeast (Schizosaccharomyces pombe)

- BNGH420024870//C2 domain// C2 domain// C2 domain
 BRACE20007330//RING CANAL PROTEIN (KELCH PROTEIN).
 BRACE20052430//Homo sapiens AMSH mRNA, complete cds.
 BRACE20054600//Xenopus laevis mRNA for Kielin, complete cds.
- 5 BRACE20059810//TSC-22/dlp/bun family
 BRACE20063540//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).
 BRACE20079200//Xenopus laevis mRNA for Kielin, complete cds.
 BRAMY20016780//Protein convertase P-domain
 BRAMY20023640//UBX domain
- 10 BRAMY20045420//Domain found in Dishevelled, Egl-10, and Pleckstrin
 BRAMY20056840//UBE-1c2
 BRAMY20063750//Homo sapiens HRIHFB2007 mRNA, partial cds.
 BRAMY20102900//Homo sapiens RU1 (RU1) mRNA, complete cds.
 BRAMY20158550//CALMODULIN.
- 15 BRAMY20223010//Mus musculus leucine-rich glioma-inactivated 1 protein precursor, (Lgi1) mRNA, complete cds.
 BRAMY20238630//TETRATRICOPEPTIDE REPEAT PROTEIN 4.
 BRAMY20245760//Araneus diadematus fibroin-4 mRNA, partial cds.
 BRAWH20047790//HMG (high mobility group) box
 BRSSN20005610//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
- 20 BRSSN20005660//Bacterial type II secretion system protein
 BRSSN20093890//Homo sapiens mRNA for Kelch motif containing protein, complete cds.
 CTONG20041150//Streptomyces ansochromogenes strain 7100 SanE (sanE) gene, complete cds.
 CTONG20066110//Homo sapiens DEME-6 mRNA, partial cds.
- 25 CTONG20069420//Ribosomal protein S14p/S29e
 CTONG20071040//BETA CRYSTALLIN B2 (BP).
 CTONG20074170//DENN (AEX-3) domain
 CTONG20083430//Nuclear transition protein 2
 CTONG20170940//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
- 30 CTONG20174290//TRICHOHYALIN.
 CTONG20174580//Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein complete cds.
 CTONG20180690//Collagen triple helix repeat (20 copies)
 CTONG20186550//cca3 protein - rat
 CTONG20188080//TPR Domain
- 35 FCBBF10004760//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
 FCBBF20033360//RING CANAL PROTEIN (KELCH PROTEIN).
 FCBBF20041380//SAM domain (Sterile alpha motif)
 FCBBF20043730//UBA domain
 FCBBF20056580//Mus musculus NSD1 protein mRNA, complete cds.
- 40 FCBBF20059660//TPR Domain
 FCBBF30019180//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A, ALPHA ISOFORM (PP2A, SUBUNIT A, PR65-ALPHA ISOFORM) (PP2A, SUBUNIT A, R1-ALPHA ISOFORM).
 FCBBF30026580//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.
 FCBBF30035570//C2 domain
- 45 FCBBF30079770//D-isomer specific 2-hydroxyacid dehydrogenases
 FCBBF30100120//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
 FCBBF30100410//Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.
 FCBBF30118890//Drosophila melanogaster La related protein (larp) mRNA, partial cds.
- 50 FCBBF30138000//trg protein - rat
 FCBBF30157270//Rattus norvegicus PAPIN mRNA, complete cds.
 FCBBF30161780//gag gene protein p24 (core nucleocapsid protein)// Zinc knuckle
 FCBBF30198670//dof protein - fruit fly (Drosophila melanogaster)
 FCBBF30222910//Mus musculus Rap2 interacting protein 8 (RPIP8) mRNA, complete cds.
- 55 FCBBF30255680//Rattus norvegicus brain specific cactin-binding protein CBP90 mRNA, partial cds.
 FCBBF30260210//Drosophila melanogaster KISMET-L long isoform (kis) mRNA, complete cds.
 FCBBF30282020//cca3 protein - rat
 FCBBF40000610//late gestation lung 2 protein [Rattus norvegicus].

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- FEBRA20029620//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 FEBRA20031150//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
 FEBRA20038330//Corticotropin-releasing factor family
 FEBRA20038970//Homo sapiens mRNA for stabilin-1 (stab1 gene).
 5 FEBRA20088610//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).
 FEBRA20150420//HYPOTHETICAL 131.5 KDA PROTEIN C02F12.7 IN CHROMOSOME X.
 FEBRA20175330//D-isomer specific 2-hydroxyacid dehydrogenases
 HEART10001420//Mus musculus skm-BOP1 (Bop) mRNA, complete cds.
 HLUNG20024050//Rubredoxin
 10 HLUNG20030420//Mus musculus mRNA for MAIL, complete cds.
 HLUNG20030490//Ambystoma tigrinum RPE65 protein mRNA, complete cds.
 HLUNG20033060//Homo sapiens GAP-like protein (N61) mRNA, complete cds.
 HLUNG20041590//ubiquitous tetratricopeptide containing protein RoXaN [Homo sapiens].
 HLUNG20045340//MOB2 PROTEIN (MPS1 BINDER 2).
 15 HLUNG20051330//FHIPEP family
 HLUNG20070410//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
 HLUNG20072100//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds.
 HLUNG20083480//Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52.
 KIDNE20027980//SAM domain (Sterile alpha motif)
 20 KIDNE20084730//Homo sapiens FH1/FH2 domain-containing protein FHOS (FHOS) mRNA, complete cds.
 KIDNE20149780//NG28 [Mus musculus]
 KIDNE20154330//Rattus norvegicus mRNA for multi PDZ domain protein.
 KIDNE20170400//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Protein kinase C terminal do-
 main// Rubredoxin
 25 KIDNE20189890//Homo sapiens mRNA for KARP-1-binding protein 2 (KAB2), complete cds.
 LIVER20010760//Homo sapiens C-type lectin-like receptor-1 mRNA, complete cds.
 LIVER20040740//RETINAL-BINDING PROTEIN (RALBP).
 MESAN20009090//Homo sapiens CEGP1 protein (CEGP1), mRNA
 MESAN20026870//PAN domain// TBC domain
 30 MESAN20090190//CEGP1 protein [Homo sapiens].
 NT2NE20059680//Homo sapiens integrin cytoplasmic domain associated protein (Icap-1a) mRNA, complete cds.
 NT2NE20077270//Adenovirus EB1 55K protein / large t-antigen
 NT2NE20087850//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
 NT2NE20095230//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.
 35 NT2NE20108420//KES1 PROTEIN.
 NT2NE20173970//Rattus norvegicus beta-catenin binding protein mRNA, complete cds.
 NT2NE20177210//Leishmania major partial ppg1 gene for proteophosphoglycan.
 NT2RP70012830//CALPHOTIN.
 NT2RP70035110//Caenorhabditis elegans UNC-89 (unc-89) gene, complete cds.
 40 NTONG20002230//Mus musculus RW1 protein mRNA, complete cds.
 NTONG20005310//Ribosomal protein S9/S16
 NTONG20029850//CALCYPHOSINE (R2D5 ANTIGEN).
 NTONG20035150//RING CANAL PROTEIN (KELCH PROTEIN).
 NTONG20058220//Homo sapiens phosphoprotein pp75 mRNA, partial cds.
 45 OCBBF20005220//Rattus norvegicus Fos-related antigen mRNA, complete cds.
 OCBBF20011860//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.
 OCBBF20016810//enhancer of polycomb [Mus musculus]
 OCBBF20147070//DNA polymerase (viral) C-terminal domain
 OCBBF20160380//liver stage antigen LSA-1 - Plasmodium falciparum
 50 OCBBF20177910//Corticotropin-releasing factor family
 PEBLM20005020//Virion host shutoff protein
 PLACE60055460//Homo sapiens leucine-zipper protein FKSG13 (FKSG13) mRNA, complete cds.
 PLACE60068710//SUPPRESSOR PROTEIN SRP40.
 PLACE60080360//mucin [Homo sapiens]
 55 PLACE60082850//Pathogenesis-related protein Bet v I family
 PLACE60098350//Human hepatocellular carcinoma associated protein (JCL-1) mRNA, complete cds.
 PLACE60105680//Homo sapiens mRNA for TU12B1-TY, complete cds.
 PLACE60119700//Homo sapiens mRNA for ABP32, complete cds.

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- PLACE60120280//SER/THR-RICH PROTEIN T10 IN DGCR REGION.
 PLACE60132200//TRICHOHYALIN.
 PLACE60181870//Pentaxin family
 PROST20084470//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds.
 5 PROST20087240//gag gene protein p24 (core nucleocapsid protein)
 PROST20122490//Gallus gallus syndesmos mRNA, complete cds.
 PROST20130320//S-100/ICaBP type calcium binding domain
 PROST20152870//Homo sapiens APC2 gene, exon 14.
 PUAEN10001640//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.
 10 PUAEN20000800//Bleomycin resistance protein
 SMINT20012220//Collagen triple helix repeat (20 copies)
 SMINT20035510//Drosophila melanogaster La related protein (Iarp) mRNA, partial cds.
 SMINT20036440//Drosophila melanogaster epsin-like protein mRNA, complete cds.
 SMINT20038660//Homo sapiens HNOEL-iso (HNOEL-iso) mRNA, complete cds.
 15 SMINT20043390//Ras association (RalGDS/AF-6) domain
 SMINT20048720//Cytochrome P450// Cytochrome P450
 SMINT20052130//Rattus norvegicus mRNA for gankyrin homologue, complete cds.
 SMINT20054050//ABC1 PROTEIN HOMOLOG PRECURSOR.
 SPLEN20024770//Rattus norvegicus (rsec6) mRNA, complete cds.
 20 SPLEN20040780//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
 SPLEN20041810//BC-2 protein [Homo sapiens]
 SPLEN20100040//258.1 KDA PROTEIN C210RF5 (KIAA0933).
 SPLEN20104150//Ribosomal protein L36
 SPLEN20116720//Homo sapiens misato mRNA, partial cds.
 25 SPLEN20176130//Homo sapiens mRNA for ALEX1, complete cds.
 SPLEN20181570//TRICHOHYALIN.
 TESTI20004310//TRICHOHYALIN.
 TESTI20016970//TPR Domain
 TESTI20030440//TRICHOHYALIN.
 30 TESTI20043180//mouse mRNA for megakaryocyte potentiating factor, complete cds.
 TESTI20043910//IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
 TESTI20044900//Strongylocentrotus purpuratus radial spokehead mRNA, complete cds.
 TESTI20046110//Extracellular link domain
 35 TESTI20047930//Homo sapiens NY-REN-2 antigen mRNA, complete cds.
 TESTI20049410//Proprotein convertase P-domain
 TESTI20053950//IQ calmodulin-binding motif
 TESTI20054700//Streptococcus pneumoniae strain g375 surface protein PspC (pspC) gene, pspC-8.1 allele, complete cds.
 40 TESTI20055880//Serum amyloid A protein
 TESTI20056030//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.
 TESTI20061090//Keratin, high sulfur B2 protein
 TESTI20064370//TPR Domain// TPR Domain// TPR Domain// TPR Domain// Synaptobrevin
 TESTI20084250//OXYSTEROL-BINDING PROTEIN.
 45 TESTI20092170//ENV polyprotein (coat polyprotein)
 TESTI20116050//UBX domain
 TESTI20120500//Kelch motif// Kelch motif
 TESTI20126280//Mus musculus STAP mRNA for sperm tail associated protein, complete cds.
 TESTI20144390//TESTIS-SPECIFIC PROTEIN PBS13.
 50 TESTI20165990//Ribosomal protein L36
 TESTI20169500//HYPOTHETICAL 51.9 KDA PROTEIN C27F1.04C IN CHROMOSOME I.
 TESTI20170280//Flagellar L-ring protein
 TESTI20176450//thioredoxin interacting factor [Mus musculus].
 TESTI20179230//Dihydropyridine sensitive L-type calcium channel (Beta subunit)
 55 TESTI20180600//Homo sapiens HOM-TES-85 tumor antigen mRNA, complete cds.
 TESTI20209050//HYPOTHETICAL 113.1 KDA PROTEIN IN PRE5-FET4 INTERGENIC REGION.
 TESTI20210570//RETINAL-BINDING PROTEIN (RALBP).
 TESTI20215310//Homo sapiens calcyclin binding protein mRNA, complete cds.

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- TESTI20247440//Human BLu protein testis isoform (BLu) mRNA, complete cds.
 TESTI20249360//Homo sapiens DME-6 mRNA, partial cds.
 TESTI20250220//TRICHOHYALIN.
 TESTI20251440//Rattus norvegicus (rsec6) mRNA, complete cds.
 5 TESTI20255460//Mus musculus mRNA for MIWI (piwi), complete cds.
 THYMU20009500//TPR Domain
 THYMU20010180//MOB1 PROTEIN (MPS1 BINDER 1).
 THYMU20013810//Human SEC7 homolog Tic (TIC) mRNA, complete cds.
 THYMU20018250//TPR Domain
 10 THYMU20026950//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.
 THYMU20028410//Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.
 THYMU20030460//Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA, complete cds.
 THYMU20031330//Homo sapiens putative nucleotide binding protein mRNA, complete cds.
 THYMU20052460//PHORBOLIN I (FRAGMENTS).
 15 THYMU20055450//Zona pellucida-like domain
 THYMU20083830//Homo sapiens angiostatin binding protein 1 mRNA, complete cds.
 THYMU20139160//Uncharacterized protein family UPF0031
 THYMU20151610//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.
 TRACH20093400//TRICHOHYALIN.
 20 TRACH20104510//Uncharacterized protein family UPF0005
 TRACH20122980//HYPOTHETICAL PROTEIN MJ0798.
 TRACH20139280//PX domain
 TRACH20164820//D-isomer specific 2-hydroxyacid dehydrogenases
 TRACH20165540//Human alpha-1 type I collagen gene surrounding osteogenesis imperfecta OI type II deletion.
 25 UTERU20051790//guanylate kinase-interacting protein 1 Maguin-1, membrane-associated - rat
 UTERU20083020//Domain of unknown function DUF71
 UTERU20121140//Rhodanese-like domain
 UTERU20128560//126.4 KDA PROTEIN IN RUVC-ASPS INTERGENIC REGION.
 UTERU20132620//AXONEME-ASSOCIATED PROTEIN MST101(2).
 30 UTERU20134830//pellino (Drosophila) homolog 2 [Homo sapiens]
 UTERU20181270//Zinc knuckle
[0266] With respect to the remaining 613 clones, there are so far no information available for estimating their functions. However, there is the possibility that the functions of these clones will be revealed in future. Their Clone Names are indicated below.
 35 ADRGL20027530, ADRGL20040310, ADRGL20040770, ADRGL20046760, ADRGL20047080, ADRGL20057560,
 ADRGL20067320, ADRGL20095330, ASTRO20003720, ASTRO20004820, ASTRO20012270, ASTRO20020350,
 ASTRO20022020, ASTRO20027330, ASTRO20047510, ASTRO20069200, ASTRO20076660, ASTRO20091770,
 ASTRO20141740, BNGH410000570, BNGH420014060, BNGH420040760, BNGH420042910, BNGH420045380,
 BNGH420061350, BNGH420062340, BNGH420085100, BRACE20009050, BRACE20017790, BRACE20018810,
 40 BRACE20025820, BRACE20038920, BRACE20054480, BRACE20057870, BRACE20059110, BRACE20062580,
 BRACE20069440, BRACE20098860, BRACE20196960, BRACE20200970, BRACE20205840, BRACE20207420,
 BRACE20212450, BRACE20216700, BRACE20219360, BRAMY10000980, BRAMY20000210, BRAMY20000250,
 BRAMY20020440, BRAMY20021580, BRAMY20023390, BRAMY20036530, BRAMY20036810, BRAMY20039290,
 BRAMY20043520, BRAMY20050640, BRAMY20052440, BRAMY20073080, BRAMY20074110, BRAMY20074860,
 45 BRAMY20076130, BRAMY20076530, BRAMY20095080, BRAMY20095570, BRAMY20100680, BRAMY20107980,
 BRAMY20120170, BRAMY20124970, BRAMY20125170, BRAMY20126910, BRAMY20139750, BRAMY20155500,
 BRAMY20159250, BRAMY20160020, BRAMY20173480, BRAMY20219620, BRAMY20225250, BRAMY20227230,
 BRAMY20227960, BRAMY20243120, BRAMY20245350, BRAMY20267780, BRAMY20269040, BRAMY20271140,
 BRAMY20287400, BRAWH20020600, BRAWH20025490, BRAWH20027250, BRAWH20055240, BRAWH20055780,
 50 BRAWH20058120, BRAWH20078080, BRAWH20082550, BRAWH20173790, BRAWH20175230, BRAWH20175340,
 BRAWH20182670, BRAWH20186010, BRCOC10000400, BRHIP20003590, BRHIP20005060, BRSSN20092440,
 CTONG10000090, CTONG20000340, CTONG20002790, CTONG20008460, CTONG20015240, CTONG20020660,
 CTONG20027660, CTONG20031150, CTONG20031890, CTONG20033500, CTONG20035240, CTONG20036800,
 CTONG20039370, CTONG20050490, CTONG20055670, CTONG20057750, CTONG20057950, CTONG20061290,
 55 CTONG20062730, CTONG20065240, CTONG20073990, CTONG20074740, CTONG20076230, CTONG20081840,
 CTONG20133720, CTONG20165590, CTONG20166580, CTONG20168460, CTONG20169530, CTONG20174440,
 CTONG20179390, CTONG20179980, CTONG20180620, CTONG20181350, CTONG20184130, CTONG20186140,
 CTONG20190630, DFNES20032550, DFNES20088810, FCBBF10002200, FCBBF20021110, FCBBF20028980,

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FCBBF20038230, FCBBF20038950, FCBBF20061310, FCBBF20070800, FCBBF30000010, FCBBF30001020,
 FCBBF30001150, FCBBF30002330, FCBBF30004730, FCBBF30005180, FCBBF30019240, FCBBF30056980,
 FCBBF30063990, FCBBF30068210, FCBBF30072480, FCBBF30074530, FCBBF30074620, FCBBF30081000,
 FCBBF30088700, FCBBF30089380, FCBBF30091010, FCBBF30099490, FCBBF30101240, FCBBF30101300,
 5 FCBBF30105080, FCBBF30106950, FCBBF30107330, FCBBF30114180, FCBBF30115230, FCBBF30128420,
 FCBBF30130580, FCBBF30151190, FCBBF30170710, FCBBF30179180, FCBBF30181730, FCBBF30194370,
 FCBBF30195700, FCBBF40001920, FCBBF40005000, FCBBF50000410, FEBRA20035200, FEBRA20039070,
 FEBRA20040260, FEBRA20040290, FEBRA20076200, FEBRA20078180, FEBRA20082660, FEBRA20083410,
 FEBRA20086600, FEBRA20091620, FEBRA20093270, FEBRA20093280, FEBRA20095410, FEBRA20098040,
 10 FEBRA20101410, FEBRA20108020, FEBRA20108580, FEBRA20121200, FEBRA20163980, FEBRA20175020,
 FEBRA20180510, FEBRA20187460, HHDPC20082970, HLUNG20009260, HLUNG20009550, HLUNG20010130,
 HLUNG20011440, HLUNG20012140, HLUNG20020500, HLUNG20021450, HLUNG20023030, HLUNG20025620,
 HLUNG20029420, HLUNG20030610, HLUNG20031620, HLUNG20033310, HLUNG20037140, HLUNG20037780,
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 15 HLUNG20065700, HLUNG20067810, HLUNG20072190, HLUNG20072450, HLUNG20079310, HLUNG20083840,
 HLUNG20083960, HLUNG20093030, HLUNG20094130, KIDNE20011600, KIDNE20024380, KIDNE20086970,
 KIDNE20091090, KIDNE20094260, KIDNE20095530, KIDNE20137310, KIDNE20138450, KIDNE20141120,
 KIDNE20142680, KIDNE20154830, KIDNE20155980, KIDNE20157100, KIDNE20176030, KIDNE20181670,
 KIDNE20191870, LIVER20007690, LIVER20032340, MESAN20008940, MESAN20021860, MESAN20029780,
 20 MESAN20030390, MESAN20041380, MESAN20045750, MESAN20060220, MESAN20085360, MESAN20089260,
 MESAN20094180, NESOP20005040, NT2NE20028700, NT2NE20033150, NT2NE20045190, NT2NE20047870,
 NT2NE20062880, NT2NE20066590, NT2NE20070520, NT2NE20073650, NT2NE20077860, NT2NE20086070,
 NT2NE20088030, NT2NE20104000, NT2NE20107810, NT2NE20112210, NT2NE20114850, NT2NE20123610,
 NT2NE20124570, NT2NE20126030, NT2NE20140280, NT2NE20148690, NT2NE20149500, NT2NE20150610,
 25 NT2NE20157120, NT2NE20165190, NT2NE20181760, NT2NE20184720, NT2RP70022820, NT2RP70049610,
 NT2RP70056290, NT2RP70074800, NT2RP70080150, NT2RP70084540, NTONG20017620, NTONG20049180,
 OCBBF20001780, OCBBF20009820, OCBBF20109450, OCBBF20112320, OCBBF20115360, OCBBF20117220,
 OCBBF20119810, OCBBF20142290, OCBBF20152330, OCBBF20188280, PLACE60001910, PLACE60011180,
 PLACE60017120, PLACE60055350, PLACE60062870, PLACE60063940, PLACE60069880, PLACE60072390,
 30 PLACE60072420, PLACE60077870, PLACE60081260, PLACE60088240, PLACE60092280, PLACE60092370,
 PLACE60095240, PLACE60109910, PLACE60132320, PLACE60132880, PLACE60155910, PLACE60157310,
 PLACE60162100, PLACE60175640, PLACE60177910, PROST10001360, PROST10002150, PROST20011800,
 PROST20014140, PROST20014650, PROST20015400, PROST20022120, PROST20036280, PROST20041460,
 PROST20042700, PROST20047440, PROST20048770, PROST20052720, PROST20054660, PROST20060200,
 35 PROST20078710, PROST20093470, PROST20094000, PROST20097310, PROST20097360, PROST20102500,
 PROST20103820, PROST20121570, PROST20124000, PROST20125420, PROST20138730, PROST20156360,
 PROST20159320, SKMUS20026340, SKMUS20064810, SKNSH10001010, SKNSH20007160, SKNSH20040390,
 SKNSH20068220, SMINT20011830, SMINT20013970, SMINT20014610, SMINT20017310, SMINT20021260,
 SMINT20023110, SMINT20031280, SMINT20045830, SMINT20045890, SMINT20047290, SMINT20056240,
 40 SMINT20067080, SMINT20070620, SMINT20077920, SMINT20084910, SMINT20085310, SMINT20085450,
 SMINT20089220, SMINT20092120, SMINT20093630, SMINT20094150, SPLEN20005160, SPLEN20005370,
 SPLEN20012450, SPLEN20015030, SPLEN20016500, SPLEN20019120, SPLEN20020530, SPLEN20023430,
 SPLEN20024510, SPLEN20029170, SPLEN20036780, SPLEN20043430, SPLEN20043460, SPLEN20045550,
 SPLEN20051420, SPLEN20062830, SPLEN20067010, SPLEN20076190, SPLEN20081640, SPLEN20087370,
 45 SPLEN20087860, SPLEN20108460, SPLEN20110210, SPLEN20111450, SPLEN20114190, SPLEN20117580,
 SPLEN20126110, SPLEN20137530, SPLEN20192570, SPLEN20193750, SPLEN20197090, SPLEN20197740,
 SPLEN20199850, SPLEN20200070, SPLEN20200340, SPLEN20203590, SPLEN20205120, TESOP10001600,
 TESTI10000850, TESTI20005980, TESTI20012360, TESTI20019590, TESTI20028020, TESTI20030610,
 TESTI20034750, TESTI20035330, TESTI20040850, TESTI20045740, TESTI20049990, TESTI20050170,
 50 TESTI20052670, TESTI20053800, TESTI20059330, TESTI20059370, TESTI20059790, TESTI20060150,
 TESTI20060450, TESTI20062180, TESTI20062580, TESTI20064990, TESTI20066170, TESTI20066280,
 TESTI20066590, TESTI20067350, TESTI20068940, TESTI20076920, TESTI20079060, TESTI20080460,
 TESTI20083890, TESTI20085670, TESTI20089290, TESTI20090180, TESTI20090970, TESTI20091360,
 TESTI20093900, TESTI20094620, TESTI20097270, TESTI20107340, TESTI20113150, TESTI20117500,
 55 TESTI20118460, TESTI20122440, TESTI20124440, TESTI20125440, TESTI20132680, TESTI20134010,
 TESTI20134270, TESTI20142480, TESTI20151050, TESTI20152490, TESTI20159380, TESTI20161010,
 TESTI20165680, TESTI20167580, TESTI20170690, TESTI20170890, TESTI20173110, TESTI20179510,
 TESTI20182210, TESTI20184280, TESTI20184820, TESTI20192570, TESTI20193520, TESTI20197290,

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TESTI20198600, TESTI20199980, TESTI20200120, TESTI20200840, TESTI20205150, TESTI20211380,
 TESTI20219390, TESTI20221790, TESTI20223380, TESTI20248850, TESTI20254090, TESTI20254480,
 TESTI20259200, TESTI20260140, TESTI20265150, TESTI20265340, TESTI20265890, TESTI20269250,
 TESTI20269360, TESTI20272380, TESTI20277300, TESTI20287760, THYMU20007750, THYMU20008000,
 5 THYMU20009460, THYMU20009710, THYMU20010710, THYMU20012560, THYMU20014430, THYMU20018390,
 THYMU20019000, THYMU20020370, THYMU20021540, THYMU20029830, THYMU20036500, THYMU20043440,
 THYMU20043560, THYMU20044100, THYMU20044520, THYMU20051340, THYMU20058550, THYMU20060480,
 THYMU20062520, THYMU20064680, THYMU20069130, THYMU20069460, THYMU20069650, THYMU20071460,
 THYMU20072580, THYMU20073070, THYMU20073080, THYMU20078020, THYMU20080490, THYMU20083500,
 10 THYMU20084520, THYMU20086430, THYMU20089170, THYMU20089900, THYMU20091040, THYMU20112570,
 THYMU20115730, THYMU20117850, THYMU20128910, THYMU20129020, THYMU20130470, THYMU20134260,
 THYMU20140510, THYMU20148010, THYMU20149230, THYMU20157620, THYMU20174490, THYMU20174790,
 THYMU20175260, THYMU20177070, THYMU20181890, THYMU20187210, TKIDN10001710, TRACH20012490,
 TRACH20021000, TRACH20025370, TRACH20026640, TRACH20041090, TRACH20044990, TRACH20049500,
 15 TRACH20051590, TRACH20057200, TRACH20080810, TRACH20093480, TRACH20101590, TRACH20123870,
 TRACH20124970, TRACH20125620, TRACH20129180, TRACH20140180, TRACH20158240, TRACH20160800,
 TRACH20174980, TRACH20182780, TRACH20185120, UTERU10001870, UTERU20000230, UTERU20011760,
 UTERU20013890, UTERU20027360, UTERU20029930, UTERU20031350, UTERU20040370, UTERU20040390,
 20 UTERU20040730, UTERU20041970, UTERU20065470, UTERU20079240, UTERU20090940, UTERU20091470,
 UTERU20102260, UTERU20103040, UTERU20106510, UTERU20140010, UTERU20167570, UTERU20173030,
 UTERU20176230

EXAMPLE 7

Expression frequency analysis *in silico*

[0267] The cDNA libraries derived from various tissues and cells as indicated in Example 1 were prepared, and cDNA clones were selected from each library at random. The 5'-end sequences were determined and the database was constructed based on the data. The database was constructed based on the nucleotide sequences of 770,546 clones, and thus the population of the database is large enough for the analysis.

[0268] Then, clones having a homologous sequence are categorized into a single cluster (clustering) by searching the nucleotide sequences of respective clones in this database with the program of nucleotide sequence homology search; the number of clones belonging to each cluster was determined and normalized for every library; thus, the ratio of a certain gene in each cDNA library was determined. This analysis gave the information of the expression frequency of genes in tissues and cells which were sources of the cDNA libraries.

[0269] Then, in order to analyze the expression of a gene containing the nucleotide sequence of the cDNA of the present invention in tissues and cells, the library derived from a tissue or a cell used in the large-scale cDNA analysis was subjected to the comparison of the expression levels between tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues and/or cells for which the nucleotide sequences of 600 or more cDNA clones had been analyzed. By this analysis, some of the genes were revealed to be involved in the pathology and functions indicated below. Each value in Tables 3 to 39 shown below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0270] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0271] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the two cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were the following clones (Table 3).

ASTRO20010290, BRAMY20036530, BRAMY20043630, BRAMY20089770, BRAMY20190550, CD34C20001750,

FCBBF20066340, FEBRA20040290, HLUNG20015180, HLUNG20041590, HLUNG20052300, KIDNE20084040, MESAN20021860, MESAN20027240, NTONG20055200, PROST20016760, PUAEN10001640, SMINT20006020, SMINT20028840, SMINT20035050, SPLEN20181570, TESTI20064530, TESTI20210030, THYMU20029830, THYMU20139160, TRACH20051590

5 [0272] These genes are involved in osteoporosis.

Genes involved in neural cell differentiation

10 [0273] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

15 [0274] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were the following clones (Table 4).

20 ADRGL20023920, ASTRO20009140, BNGH420077980, BNGH420086030, BRACE20062580, BRACE20079370, BRACE20215410, BRAMY20003540, BRAMY20043630, BRAMY20076130, BRAMY20095080, BRAMY20227860, BRAWH20082550, BRHIP10001040, BRSSN20005610, CTONG20027660, CTONG20044230, CTONG20066110, CTONG20079590, CTONG20084660, CTONG20133720, CTONG20165750, CTONG20188080, FCBBF20023490, FCBBF20033360, FCBBF20059660, FCBBF20070950, FCBBF30004340, FCBBF30095410, FCBBF30125460, FCBBF30179180, FCBBF30236670, FCBBF30257370, FCBBF50000610, FCBBF50001650, FEBRA20038330, FEBRA20039260, FEBRA20063720, FEBRA20090220, FEBRA20150420, HEART10001490, HLUNG20032460, HLUNG20041590, KIDNE20089870, MESAN20016270, MESAN20021860, MESAN20060430, MESAN20067430, NT2NE20018740, NT2NE20018890, NT2NE20021860, NT2NE20026200, NT2NE20026510, NT2NE20028700, NT2NE20033150, NT2NE20037050, NT2NE20038870, NT2NE20039210, NT2NE20042550, NT2NE20045190, NT2NE20047870, NT2NE20053230, NT2NE20053950, NT2NE20059210, NT2NE20059680, NT2NE20060750, NT2NE20061030, NT2NE20062880, NT2NE20064780, NT2NE20066590, NT2NE20069580, NT2NE20070520, NT2NE20073650, NT2NE20077250, NT2NE20077270, NT2NE20077860, NT2NE20079670, NT2NE20080770, NT2NE20082130, NT2NE20082600, NT2NE20086070, NT2NE20087270, NT2NE20087850, NT2NE20088030, NT2NE20092950, NT2NE20095230, NT2NE20104000, NT2NE20107810, NT2NE20108420, NT2NE20111190, NT2NE20112210, NT2NE20114850, NT2NE20117580, NT2NE20119980, NT2NE20123610, NT2NE20124570, NT2NE20126030, NT2NE20127900, NT2NE20140130, NT2NE20140280, NT2NE20141040, NT2NE20145250, NT2NE20146510, NT2NE20148690, NT2NE20149500, NT2NE20150610, NT2NE20152620, NT2NE20153620, NT2NE20155650, NT2NE20157120, NT2NE20165190, NT2NE20167660, NT2NE20173970, NT2NE20177210, NT2NE20181760, NT2NE20181800, NT2NE20184720, NT2RI20016240, NT2RI20021200, NT2RI20033920, NT2RI20093010, NT2RP70001120, NT2RP70001730, NT2RP70003110, NT2RP70012830, NT2RP70022820, NT2RP70027790, NT2RP70029780, NT2RP70030840, NT2RP70031070, NT2RP70031340, NT2RP70031480, NT2RP70035110, NT2RP70046410, NT2RP70049610, NT2RP70056290, NT2RP70056690, NT2RP70057500, NT2RP70064570, NT2RP70074800, NT2RP70075300, NT2RP70075800, NT2RP70080150, NT2RP70084540, NT2RP70087140, NT2RP70090870, OCBBF20001780, OCBBF20009820, OCBBF20142290, OCBBF20155030, OCBBF20175360, OCBBF20177540, OCBBF20177910, PLACE60054820, PLACE60061370, PLACE60073090, PLACE60162100, PROST20011800, PROST20045700, PROST20078710, PROST20094000, PUAEN10000650, PUAEN10001640, SKNMC20006350, SMINT20016150, SMINT20030740, SMINT20035510, SMINT20039050, SMINT20047290, SPLEN20063250, SPLEN20117580, SPLEN20125230, TESTI20030610, TESTI20043910, TESTI20066280, TESTI20067480, TESTI20105130, TESTI20106170, TESTI20143180, TESTI20221790, TESTI20254090, TESTI20274960, THYMU10004280, THYMU20007020, THYMU20104480, THYMU20139160, TRACH20026640, UTERU10001060, UTERU20026620, UTERU20079240, UTERU20083020, UTERU20102260, UTERU20132620

50 [0275] These genes are neurological disease-related genes.

Cancer-related genes

55 [0276] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression can contribute to the carcinogenesis in tissues and cells. Thus, the genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0277] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast

(BEAST) showed that the genes whose expression levels were different between the two were the following clones (Table 5).

CTONG20070780, CTONG20084660, HLUNG20045340, TESTI20047370

[0278] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were the following clones (Table 6).

SMINT20030740

[0279] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were the following clones (Table 7).

UTERU2004037

[0280] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were the following clones (Table 8).

HLUNG20015180, NESOP20004520, NESOP20005040, TESOP10000350, TESOP10001600, THYMU20071120

[0281] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 9).

ASTRO20009140, ASTRO20027330, ASTRO20055930, BGGI120010750, BNGH420074600, BRACE20050870, BRACE20054480, BRACE20062580, BRACE20219360, BRAMY20003540, BRAMY20003880, BRAMY20043630, BRAMY20055760, BRAMY20125360, BRAMY20190550, BRAMY20204270, BRAMY20227860, BRAWH20014590, BRAWH20093070, BRHIP10001040, CTONG20033750, CTONG20039370, CTONG20045500, CTONG20079590, FCBBF20023490, FCBBF30004340, FCBBF30106950, FCBBF30115230, FCBBF30169280, FCBBF30225930, FCBBF30282020, FEBRA20038330, FEBRA20039260, FEBRA20040290, FEBRA20082660, FEBRA20121200, FEBRA20170240, HEART10001490, HLUNG20041590, HLUNG20068120, HLUNG20072450, HLUNG20083480, HLUNG20083960, KIDNE20011600, KIDNE20016360, KIDNE20024380, KIDNE20027980, KIDNE20080690, KIDNE20081170, KIDNE20083150, KIDNE20083620, KIDNE20084030, KIDNE20084040, KIDNE20084730, KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20086970, KIDNE20087880, KIDNE20088240, KIDNE20089870, KIDNE20091090, KIDNE20094260, KIDNE20094670, KIDNE20095530, KIDNE20133460, KIDNE20133880, KIDNE20134130, KIDNE20134890, KIDNE20137310, KIDNE20138450, KIDNE20140870, KIDNE20141120, KIDNE20141700, KIDNE20142680, KIDNE20142680, KIDNE20142900, KIDNE20143200, KIDNE20147170, KIDNE20148080, KIDNE20149780, KIDNE20150730, KIDNE20152440, KIDNE20154330, KIDNE20154830, KIDNE20155980, KIDNE20157100, KIDNE20160360, KIDNE20160960, KIDNE20163710, KIDNE20165390, KIDNE20169180, KIDNE20170400, KIDNE20173150, KIDNE20173430, KIDNE20176030, KIDNE20181670, KIDNE20182540, KIDNE20186170, KIDNE20188630, KIDNE20189890, KIDNE20189960, KIDNE20191870, MESAN20038520, MESAN20041380, OCBBF20016390, OCBBF20142290, OCBBF20174890, PLACE60061370, PLACE60073090, PLACE60181870, PROST20016760, PUAEN10000650, SMINT20039050, SMINT20089210, SPLEN20017610, SPLEN20024930, SPLEN20057830, SPLEN20063250, SPLEN20126110, SPLEN20135030, SPLEN20136700, TESTI20070740, TESTI20262150, THYMU20009500, THYMU20019260, THYMU20157620, TKIDN10000620, TKIDN10001710, TKIDN10001920, TRACH20011010, UMVEN10001380

[0282] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were the following clones (Table 10).

CTONG20069320, FCBBF30236670, FEBRA20038220, FEBRA20039260, KIDNE20087880, LIVER20006260, LIVER20007690, LIVER20007750, LIVER20010510, LIVER20010760, LIVER20010990, LIVER20011640, LIVER20013890, LIVER20026440, LIVER20030650, LIVER20032340, LIVER20038000, LIVER20040740, LIVER20055270, MESAN20027240, NT2RI20021200, SKMUS20006790, TESTI20035330, THYMU10004280, THYMU20029830

[0283] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 11).

HLUNG20052300, SMINT20035050, HLUNG20041590, PROST20016760, BRAMY20043630, HLUNG20015180, THYMU20139160, HLUNG20020850, HLUNG20032460, BRAMY20204270, BRAMY20001510, BRAMY20227860, CTONG20029030, CTONG20168460, CTONG20186290, FEBRA20039260, FEBRA20078800, FEBRA20163980, HCHON20000870, HLUNG20008460, HLUNG20009260, HLUNG20009550, HLUNG20010130, HLUNG20011260, HLUNG20011440, HLUNG20011460, HLUNG20012140, HLUNG20014590, HLUNG20015070, HLUNG20020500, HLUNG20021450, HLUNG20023030, HLUNG20024050, HLUNG20025620, HLUNG20028110, HLUNG20029420, HLUNG20029490, HLUNG20030420, HLUNG20030490, HLUNG20030610, HLUNG20031620, HLUNG20033060, HLUNG20033310, HLUNG20033350, HLUNG20034970, HLUNG20037140, HLUNG20037160, HLUNG20037780,

HLUNG20038330, HLUNG20041540, HLUNG20042730, HLUNG20045340, HLUNG20047070, HLUNG20050760, HLUNG20051330, HLUNG20054790, HLUNG20055240, HLUNG20056560, HLUNG20057380, HLUNG20059240, HLUNG20060670, HLUNG20063700, HLUNG20065700, HLUNG20065990, HLUNG20067810, HLUNG20068120, HLUNG20069350, HLUNG20070410, HLUNG20072100, HLUNG20072190, HLUNG20072450, HLUNG20074330, HLUNG20079310, HLUNG20081390, HLUNG20081530, HLUNG20082350, HLUNG20083330, HLUNG20083480, HLUNG20083840, HLUNG20083960, HLUNG20084790, HLUNG20085210, HLUNG20088750, HLUNG20092530, HLUNG20093030, HLUNG20094130, KIDNE20142900, PROST20052850, SKNMC20006350, SPLEN20012450, TESTI20057590, TESTI20061200, TESTI20067480, TESTI20116050, THYMU10004280, THYMU20010180, TRACH20011010, UTERU20016580, UTERU20127030

[0284] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were the following clones (Table 12).

KIDNE20089870, NT2RP70075300, TESTI20132310

[0285] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were the following clones (Table 13).

BNGH420087430, BRAMY20227860, BRAWH20027250, CTONG20174440, FEBRA20090220, PUAEN10000650, SMINT20023110, SMINT20030740, SMINT20045890, SPLEN20048800, SPLEN20139360, TESTI20063410, TESTI20150920, TRACH20026640, UTERU20041970

[0286] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were the following clones (Table 14).

ADRL20020290, BRACE20038920, BRAMY20091230, BRAMY20093490, BRAMY20227860, BRHIP20005060, CTONG20069320, CTONG20083430, FCBBF30005360, FCBBF30257370, FEBRA20038330, FEBRA20039260, FEBRA20040260, FEBRA20078180, FEBRA20087550, HLUNG20015070, HLUNG20015180, MESAN20007110, MESAN20067430, MESAN20095800, NT2RP70057500, SKMUS20008730, SKNMC20006350, SMINT20035050, SMINT20045890, SPLEN20073880, SPLEN20076470, SPLEN20118050, TESTI20030610, TESTI20035330, TESTI20057590, TESTI20059080, TESTI20105130, THYMU10004280, THYMU20139160, UTERU10001060, UTERU10001870, UTERU20000230, UTERU20000950, UTERU20011760, UTERU20013890, UTERU20016580, UTERU20026620, UTERU20027360, UTERU20029930, UTERU20031350, UTERU20035770, UTERU20040150, UTERU20040370, UTERU20040390, UTERU20040730, UTERU20041630, UTERU20041970, UTERU20045200, UTERU20051790, UTERU20064120, UTERU20065470, UTERU20079240, UTERU20083020, UTERU20086530, UTERU20087070, UTERU20087850, UTERU20089300, UTERU20089390, UTERU20089620, UTERU20090940, UTERU20091470, UTERU20094830, UTERU20095100, UTERU20099040, UTERU20099510, UTERU20101150, UTERU20102260, UTERU20103040, UTERU20103200, UTERU20104310, UTERU20106510, UTERU20121140, UTERU20122520, UTERU20125810, UTERU20127030, UTERU20127150, UTERU20128560, UTERU20132620, UTERU20134830, UTERU20139760, UTERU20140010, UTERU20167570, UTERU20168960, UTERU20169020, UTERU20173030, UTERU20176230, UTERU20177150, UTERU20181270, UTERU20185220, UTERU20188670, UTERU20188840

[0287] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were the following clones (Table 15).

ADRL20023920, BRACE20038920, BRACE20050870, BRACE20061620, BRAMY20036530, BRAMY20076130, BRAMY20204270, BRAMY20267780, BRCAN20001680, CTONG10000090, CTONG20000340, CTONG20002790, CTONG20004120, CTONG20004520, CTONG20007660, CTONG20008190, CTONG20008460, CTONG20015240, CTONG20017490, CTONG20020660, CTONG20020950, CTONG20027660, CTONG20029030, CTONG20030280, CTONG20031150, CTONG20031890, CTONG20032930, CTONG20033500, CTONG20033610, CTONG20033750, CTONG20035240, CTONG20036800, CTONG20036990, CTONG20039370, CTONG20041150, CTONG20041260, CTONG20042640, CTONG20044230, CTONG20044870, CTONG20045500, CTONG20046690, CTONG20049480, CTONG20050490, CTONG20051100, CTONG20051450, CTONG20052780, CTONG20053990, CTONG20055670, CTONG20055850, CTONG20056150, CTONG20057750, CTONG20057950, CTONG20059130, CTONG20060040, CTONG20061290, CTONG20062730, CTONG20063770, CTONG20063930, CTONG20065240, CTONG20065680, CTONG20066110, CTONG20068360, CTONG20069320, CTONG20069420, CTONG20070090, CTONG20070720, CTONG20070780, CTONG20070910, CTONG20071040, CTONG20071680, CTONG20072930, CTONG20073990, CTONG20074000, CTONG20074170, CTONG20074740, CTONG20076230, CTONG20076810, CTONG20077760, CTONG20078340, CTONG20079590, CTONG20080140, CTONG20081840, CTONG20083430, CTONG20083980, CTONG20084020, CTONG20084660, CTONG20085210, CTONG20133720, CTONG20165590, CTONG20165750, CTONG20166580, CTONG20167750, CTONG20168240, CTONG20168460, CTONG20169040, CTONG20169530,

CTONG20170940, CTONG20174290, CTONG20174580, CTONG20176040, CTONG20179390, CTONG20179890, CTONG20179980, CTONG20180620, CTONG20180690, CTONG20181350, CTONG20183430, CTONG20183830, CTONG20184130, CTONG20184830, CTONG20186140, CTONG20186290, CTONG20186370, CTONG20186520, CTONG20186550, CTONG20188080, CTONG20189000, CTONG20190290, CTONG20190630, FCBBF20070950, FCBBF30001100, FCBBF30175350, FCBBF40005000, FEBRA20027070, FEBRA20038330, FEBRA20039260, FEBRA20040290, FEBRA20046200, FEBRA20063720, FEBRA20078800, FEBRA20090220, HCHON20000870, HLUNG20068120, MESAN20008150, MESAN20027900, NT2NE20153620, NT2RP70001730, NT2RP70012830, NT2RP70027790, NT2RP70057500, NT2RP70064570, NT2RP70090870, NTONG20002230, NTONG20005310, NTONG20017620, NTONG20029850, NTONG20031580, NTONG20032100, NTONG20034540, NTONG20035150, NTONG20043080, NTONG20048440, NTONG20049180, NTONG20053630, NTONG20053730, NTONG20053910, NTONG20055200, NTONG20058010, NTONG20058220, OCBBF20110730, OCBBF20177540, OCBBF20177910, PROST20016760, PROST20042700, PROST20050390, PROST20063430, PROST20130320, PUAEN10000650, PUAEN10001640, PUAEN20003120, SKMUS20006790, SKNMC20006350, SKNSH20007160, SMINT20030740, SMINT20035510, SMINT20089210, SPLEN20024930, SPLEN20040780, SPLEN20063250, SPLEN20181570, SPLEN20187490, TESTI20047370, TESTI20057880, TESTI20064530, TESTI20079980, TESTI20105130, TESTI20118460, TESTI20121040, TESTI20197290, THYMU10004280, THYMU20030460, THYMU20055460, THYMU20089900, THYMU20121040, THYMU20139160, THYMU20145990, TRACH20011010, TRACH20090060, UTERU20000230, UTERU20000950, UTERU20016580, UTERU20045200, UTERU20083020

[0288] These genes are involved in cancers.

[0289] Further, there is a method to search for genes involved in development and differentiation: the expression frequency analysis in which the expression levels of genes are compared between developing or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0290] Search was carried out for the genes whose expression frequencies were different between developing and/or differentiating tissues and/or cells, and adult tissues and/or cells, by using the information of gene expression frequency based on the database of the nucleotide sequences of 770,546 clones shown above.

[0291] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were the following clones (Tables 16 to 36).

ADRGL20020290, ADRGL20021910, ADRGL20023920, ADRGL20046760, ADRGL20062330, ADRGL20079060, ASTRO20009140, ASTRO20020240, ASTRO20027330, ASTRO20047510, ASTRO20055530, ASTRO20055570, ASTRO20055930, ASTRO20090680, BGGI120010750, BNGH420021680, BNGH420023870, BNGH420059680, BNGH420074600, BNGH420086030, BRACE10000510, BRACE20003310, BRACE20007330, BRACE20009050, BRACE20014450, BRACE20017790, BRACE20018810, BRACE20025820, BRACE20038920, BRACE20050870, BRACE20051600, BRACE20051930, BRACE20052430, BRACE20052530, BRACE20054080, BRACE20054480, BRACE20054600, BRACE20055560, BRACE20057870, BRACE20059110, BRACE20059810, BRACE20061620, BRACE20062580, BRACE20063540, BRACE20065470, BRACE20066360, BRACE20068710, BRACE20069000, BRACE20069110, BRACE20069440, BRACE20079200, BRACE20079370, BRACE20097540, BRACE20098860, BRACE20099070, BRACE20194670, BRACE20196180, BRACE20196960, BRACE20200770, BRACE20200970, BRACE20204670, BRACE20205840, BRACE20207420, BRACE20212450, BRACE20215410, BRACE20216700, BRACE20216950, BRACE20219360, BRAMY10000980, BRAMY10001730, BRAMY20000210, BRAMY20000250, BRAMY20001510, BRAMY20003540, BRAMY20003880, BRAMY20005080, BRAMY20013670, BRAMY20016780, BRAMY20020440, BRAMY20021580, BRAMY20023390, BRAMY20023640, BRAMY20024790, BRAMY20027390, BRAMY20027990, BRAMY20028530, BRAMY20028620, BRAMY20035380, BRAMY20035830, BRAMY20036530, BRAMY20036810, BRAMY20038980, BRAMY20039290, BRAMY20040580, BRAMY20043520, BRAMY20043630, BRAMY20044920, BRAMY20045210, BRAMY20045420, BRAMY20047560, BRAMY20050640, BRAMY20050940, BRAMY20051820, BRAMY20052440, BRAMY20053910, BRAMY20055760, BRAMY20056620, BRAMY20056840, BRAMY20063750, BRAMY20072440, BRAMY20072870, BRAMY20073080, BRAMY20074110, BRAMY20074860, BRAMY20076100, BRAMY20076130, BRAMY20076530, BRAMY20083330, BRAMY20083820, BRAMY20089770, BRAMY20091230, BRAMY20093490, BRAMY20094890, BRAMY20095080, BRAMY20095570, BRAMY20096930, BRAMY20100680, BRAMY20102900, BRAMY20107980, BRAMY20111780, BRAMY20117670, BRAMY20118410, BRAMY20118490, BRAMY20120170, BRAMY20123400, BRAMY20124970, BRAMY20125170, BRAMY20125360, BRAMY20125550, BRAMY20126910, BRAMY20127310, BRAMY20127760, BRAMY20134050, BRAMY20135720, BRAMY20137360, BRAMY20139440, BRAMY20139750, BRAMY20143870, BRAMY20152510, BRAMY20155500, BRAMY20158550, BRAMY20159250, BRAMY20160020, BRAMY20173480, BRAMY20190550, BRAMY20194680, BRAMY20204270, BRAMY20206340, BRAMY20219620, BRAMY20221600, BRAMY20223010, BRAMY20225250, BRAMY20225320, BRAMY20227230, BRAMY20227860, BRAMY20227960, BRAMY20231150, BRAMY20234820,

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BRAMY20237190, BRAMY20238630, BRAMY20243120, BRAMY20244490, BRAMY20245140, BRAMY20245350,
 BRAMY20245760, BRAMY20251210, BRAMY20251750, BRAMY20263000, BRAMY20267780, BRAMY20269040,
 BRAMY20271140, BRAMY20274510, BRAMY20285650, BRAMY20287400, BRAWH20014590, BRAWH20020470,
 BRAWH20020600, BRAWH20021910, BRAWH20025490, BRAWH20026010, BRAWH20027250, BRAWH20030000,
 5 BRAWH20039640, BRAWH20040680, BRAWH20047790, BRAWH20050740, BRAWH20055240, BRAWH20055330,
 BRAWH20055780, BRAWH20058120, BRAWH20063010, BRAWH20078080, BRAWH20078620, BRAWH20080580,
 BRAWH20082550, BRAWH20082920, BRAWH20093040, BRAWH20093070, BRAWH20094900, BRAWH20095900,
 BRAWH20173790, BRAWH20174330, BRAWH20175230, BRAWH20175340, BRAWH20176850, BRAWH20182670,
 BRAWH20183170, BRAWH20185260, BRAWH20185270, BRAWH20186010, BRAWH20188750, BRAWH20190530,
 10 BRAWH20190550, BRAWH20191980, BRCAN10000760, BRCAN10001050, BRCAN10001680, BRCAN20001480,
 BRCAN20004180, BRCAN20005230, BRCAN20005410, BRCOC10000400, BRCOC20000470, BRCOC20003600,
 BRHIP10000720, BRHIP10001040, BRHIP20000210, BRHIP20003590, BRHIP20005060, BRSSN20001970,
 BRSSN20005610, BRSSN20005660, BRSSN20066440, BRSSN20074640, BRSSN20091190, BRSSN20092440,
 BRSSN20093890, CTONG20032930, CTONG20035240, CTONG20044870, CTONG20063930, CTONG20069320,
 15 CTONG20070720, CTONG20071040, CTONG20071680, CTONG20074170, CTONG20078340, CTONG20079590,
 CTONG20080140, CTONG20085210, CTONG20133720, CTONG20165750, CTONG20168240, CTONG20170940,
 CTONG20183430, CTONG20186370, CTONG20188080, FCBBF10000230, FCBBF10002200, FCBBF10004760,
 FCBBF20018680, FCBBF20020440, FCBBF20021110, FCBBF20023490, FCBBF20028980, FCBBF20029280,
 FCBBF20032930, FCBBF20033360, FCBBF20035430, FCBBF20035490, FCBBF20036360, FCBBF20038230,
 20 FCBBF20038950, FCBBF20041380, FCBBF20043730, FCBBF20054390, FCBBF20056580, FCBBF20059660,
 FCBBF20061310, FCBBF20066340, FCBBF20070800, FCBBF20070950, FCBBF30000010, FCBBF30001020,
 FCBBF30001100, FCBBF30001150, FCBBF30002270, FCBBF30002280, FCBBF30002330, FCBBF30003610,
 FCBBF30004340, FCBBF30004730, FCBBF30005180, FCBBF30005360, FCBBF30005500, FCBBF30019140,
 FCBBF30019180, FCBBF30019240, FCBBF30021900, FCBBF30022680, FCBBF30026580, FCBBF30029250,
 25 FCBBF30035570, FCBBF30042610, FCBBF30048420, FCBBF30053300, FCBBF30056980, FCBBF30062490,
 FCBBF30063990, FCBBF30068210, FCBBF30071500, FCBBF30072440, FCBBF30072480, FCBBF30074530,
 FCBBF30074620, FCBBF30075970, FCBBF30076310, FCBBF30078600, FCBBF30079770, FCBBF30080730,
 FCBBF30081000, FCBBF30085560, FCBBF30088700, FCBBF30089380, FCBBF30091010, FCBBF30091520,
 FCBBF30093170, FCBBF30095410, FCBBF30099490, FCBBF30100080, FCBBF30100120, FCBBF30100410,
 30 FCBBF30101240, FCBBF30101300, FCBBF30105080, FCBBF30105440, FCBBF30105860, FCBBF30106950,
 FCBBF30107290, FCBBF30107330, FCBBF30114180, FCBBF30114850, FCBBF30115230, FCBBF30115920,
 FCBBF30118670, FCBBF30118890, FCBBF30125460, FCBBF30125880, FCBBF30128420, FCBBF30129010,
 FCBBF30130410, FCBBF30130580, FCBBF30132050, FCBBF30132660, FCBBF30135890, FCBBF30136230,
 FCBBF30138000, FCBBF30142290, FCBBF30143550, FCBBF30145670, FCBBF30151190, FCBBF30153170,
 35 FCBBF30157270, FCBBF30161780, FCBBF30164510, FCBBF30166220, FCBBF30169280, FCBBF30169870,
 FCBBF30170710, FCBBF30171230, FCBBF30172330, FCBBF30173960, FCBBF30175350, FCBBF30177290,
 FCBBF30179180, FCBBF30179740, FCBBF30181730, FCBBF30194370, FCBBF30194550, FCBBF30195690,
 FCBBF30195700, FCBBF30197840, FCBBF30198670, FCBBF30201630, FCBBF30212210, FCBBF30215240,
 FCBBF30220050, FCBBF30222910, FCBBF30223110, FCBBF30223210, FCBBF30225930, FCBBF30228940,
 40 FCBBF30230610, FCBBF30236670, FCBBF30250980, FCBBF30255680, FCBBF30257370, FCBBF30259050,
 FCBBF30260210, FCBBF30260480, FCBBF30263080, FCBBF30266510, FCBBF30271990, FCBBF30275590,
 FCBBF30282020, FCBBF30285930, FCBBF30287940, FCBBF40000610, FCBBF40001920, FCBBF40005000,
 FCBBF50000410, FCBBF50000610, FCBBF50001650, FCBBF50003530, FCBBF50004950, FEBRA20005040,
 FEBRA20007820, FEBRA20018670, FEBRA20026820, FEBRA20027070, FEBRA20029620, FEBRA20031000,
 45 FEBRA20031150, FEBRA20031280, FEBRA20031810, FEBRA20035200, FEBRA20035240, FEBRA20038220,
 FEBRA20038330, FEBRA20038970, FEBRA20039070, FEBRA20039260, FEBRA20040230, FEBRA20040260,
 FEBRA20040290, FEBRA20040560, FEBRA20045380, FEBRA20046200, FEBRA20046280, FEBRA20046510,
 FEBRA20057010, FEBRA20063720, FEBRA20076200, FEBRA20078180, FEBRA20078800, FEBRA20080860,
 FEBRA20082660, FEBRA20083410, FEBRA20084750, FEBRA20086600, FEBRA20087550, FEBRA20088610,
 50 FEBRA20088810, FEBRA20090160, FEBRA20090220, FEBRA20091620, FEBRA20092760, FEBRA20093270,
 FEBRA20093280, FEBRA20095410, FEBRA20098040, FEBRA20099860, FEBRA20101410, FEBRA20108020,
 FEBRA20108580, FEBRA20115930, FEBRA20116650, FEBRA20121200, FEBRA20121950, FEBRA20141980,
 FEBRA20150420, FEBRA20151750, FEBRA20163980, FEBRA20170240, FEBRA20172230, FEBRA20173330,
 FEBRA20175020, FEBRA20175330, FEBRA20177800, FEBRA20180510, FEBRA20182030, FEBRA20187460,
 55 FEBRA20191720, HCHON20002650, HCHON20002710, HEART10001490, HLUNG20008460, HLUNG20011460,
 HLUNG20014590, HLUNG20015070, HLUNG20015180, HLUNG20020850, HLUNG20028110, HLUNG20031620,
 HLUNG20032460, HLUNG20033060, HLUNG20041590, HLUNG20045340, HLUNG20056560, HLUNG20068120,
 HLUNG20081390, HLUNG20083480, HLUNG20085210, HLUNG20094130, KIDNE20080690, KIDNE20084030,

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KIDNE20086660, KIDNE20094670, KIDNE20134130, KIDNE20138450, KIDNE20140870, KIDNE20149780, KIDNE20170400, KIDNE20173430, MESAN20021860, MESAN20030350, MESAN20034440, MESAN20038520, MESAN20045750, MESAN20067430, MESAN20089260, MESAN20095800, NT2NE20026200, NT2NE20033150, NT2NE20042550, NT2NE20045190, NT2NE20053950, NT2NE20061030, NT2NE20069580, NT2NE20082130, NT2NE20082600, NT2NE20088030, NT2NE20092950, NT2NE20095230, NT2NE20108420, NT2NE20111190, NT2NE20112210, NT2NE20141040, NT2NE20177210, NT2NE20181800, NT2RI20021200, NT2RP70001120, NT2RP70001730, NT2RP70012830, NT2RP70035110, NT2RP70057500, NT2RP70075300, NT2RP70087140, NT2RP70090870, NTONG20002230, NTONG20017620, NTONG20049180, NTONG20055200, OCBBF20000740, OCBBF20001780, OCBBF20005220, OCBBF20009820, OCBBF20011860, OCBBF20012520, OCBBF20016390, OCBBF20016810, OCBBF20109450, OCBBF20109780, OCBBF20110210, OCBBF20110730, OCBBF20111370, OCBBF20111600, OCBBF20112280, OCBBF20112320, OCBBF20113110, OCBBF20115360, OCBBF20116250, OCBBF20117220, OCBBF20118720, OCBBF20119810, OCBBF20120010, OCBBF20120950, OCBBF20121910, OCBBF20123200, OCBBF20142290, OCBBF20147070, OCBBF20152330, OCBBF20155030, OCBBF20156450, OCBBF20157970, OCBBF20160380, OCBBF20165900, OCBBF20165910, OCBBF20166890, OCBBF20166900, OCBBF20167290, OCBBF20170350, OCBBF20174580, OCBBF20174890, OCBBF20175360, OCBBF20176650, OCBBF20177540, OCBBF20177910, OCBBF20182060, OCBBF20185630, OCBBF20188280, OCBBF20191950, PLACE60054820, PLACE60056910, PLACE60061370, PLACE60064740, PLACE60073090, PLACE60120280, PLACE60132200, PLACE60150510, PLACE60154450, PLACE60157310, PLACE60162100, PROST10002150, PROST20014150, PROST20016760, PROST20024250, PROST20035170, PROST20035830, PROST20042700, PROST20045700, PROST20050390, PROST20054660, PROST20078710, PROST20094000, PROST20097310, PROST20097840, PROST20103820, PROST20114100, PROST20130320, PROST20151370, PUAEN10000650, PUAEN10001640, PUAEN20003120, SKNMC20006350, SKNSH10001010, SKNSH20007160, SKNSH20030640, SKNSH20094350, SMINT20000070, SMINT20002320, SMINT20030740, SMINT20039050, SMINT20045890, SMINT20047290, SMINT20048720, SMINT20056240, SMINT20077920, SMINT20088690, SMINT20089210, SMINT20089600, SMINT20094150, SPLEN20005160, SPLEN20005370, SPLEN20012450, SPLEN20024930, SPLEN20040780, SPLEN20048800, SPLEN20055600, SPLEN20057830, SPLEN20063250, SPLEN20071820, SPLEN20073880, SPLEN20076470, SPLEN20104690, SPLEN20114190, SPLEN20125230, SPLEN20135030, SPLEN20136700, SPLEN20175920, SPLEN20181570, SPLEN20183020, SPLEN20187490, SPLEN20193490, SPLEN20193790, SPLEN20197740, SPLEN20200070, SPLEN20200340, TESOP10000350, TESTI20005980, TESTI20030440, TESTI20030610, TESTI20031410, TESTI20035330, TESTI20047370, TESTI20050400, TESTI20050720, TESTI20053780, TESTI20057430, TESTI20057590, TESTI20057840, TESTI20057880, TESTI20059080, TESTI20061200, TESTI20062580, TESTI20063410, TESTI20064530, TESTI20066280, TESTI20067480, TESTI20071630, TESTI20079980, TESTI20081890, TESTI20089290, TESTI20090180, TESTI20105130, TESTI20106170, TESTI20121040, TESTI20150920, TESTI20169500, TESTI20193080, TESTI20215310, TESTI20221790, TESTI20245860, TESTI20252690, TESTI20254090, TESTI20261160, TESTI20262150, TESTI20274960, THYMU20007750, THYMU20009460, THYMU20009710, THYMU20019260, THYMU20028410, THYMU20030460, THYMU20031330, THYMU20043440, THYMU20044100, THYMU20044520, THYMU20049060, THYMU20055460, THYMU20055740, THYMU20071120, THYMU20078020, THYMU20089900, THYMU20091040, THYMU20104480, THYMU20120240, THYMU20139160, THYMU20143230, THYMU20150190, THYMU20157620, THYMU20176010, TKIDN10001920, TRACH20012490, TRACH20021000, TRACH20026640, TRACH20058000, TRACH20090060, TRACH20159390, UMVEN10001380, UTERU10001060, UTERU20000230, UTERU20000950, UTERU20026620, UTERU20041970, UTERU20065470, UTERU20079240, UTERU20083020, UTERU20089300, UTERU20089390, UTERU20095100, UTERU20102260, UTERU20103200, UTERU20127150, UTERU20128560

[0292] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were the following clones (Table 37). BRAMY20043630, BRAMY20072870, BRAMY20227860, BRAWH20093070, BRCAN10001680, FCBBF30053300, FEBRA20078800, FEBRA20090220, HCHON20000870, HEART10001420, HEART10001490, HEART20009590, HEART20019310, HEART20022200, HEART20031680, HEART20047640, HEART20063100, HEART20082570, HLUNG20083960, PLACE60088240, PLACE60120280, PROST20016760, PROST20035170, PROST20062820, PROST20127450, SKMUS20006790, SKMUS20008730, TESTI20270130

[0293] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 38). ASTRO20009140, BGGI120010750, BRACE20054480, BRACE20062580, BRACE20219360, BRAMY20001510, BRAMY20003540, BRAMY20003880, BRAMY20043630, BRAMY20204270, CTONG20033750, CTONG20039370, CTONG20045500, FCBBF20023490, FEBRA20039260, FEBRA20040290, HEART10001490, HLUNG20041590, HLUNG20068120, HLUNG20072450, HLUNG20083960, KIDNE20011600, KIDNE20016360, KIDNE20024380,

KIDNE20027980, KIDNE20080690, KIDNE20081170, KIDNE20083150, KIDNE20083620, KIDNE20084030,
 KIDNE20084040, KIDNE20084730, KIDNE20084800, KIDNE20086490, KIDNE20086660, KIDNE20086970,
 KIDNE20087880, KIDNE20088240, KIDNE20089870, KIDNE20091090, KIDNE20094260, KIDNE20094670,
 KIDNE20095530, KIDNE20133460, KIDNE20133880, KIDNE20134130, KIDNE20134890, KIDNE20137310,
 5 KIDNE20138450, KIDNE20140870, KIDNE20141120, KIDNE20141700, KIDNE20142680, KIDNE20142900,
 KIDNE20143200, KIDNE20147170, KIDNE20148080, KIDNE20149780, KIDNE20150730, KIDNE20152440,
 KIDNE20154330, KIDNE20154830, KIDNE20155980, KIDNE20157100, KIDNE20160360, KIDNE20160960,
 KIDNE20163710, KIDNE20165390, KIDNE20169180, KIDNE20170400, KIDNE20173150, KIDNE20173430,
 KIDNE20176030, KIDNE20181670, KIDNE20182540, KIDNE20186170, KIDNE20186630, KIDNE20189890,
 10 KIDNE20189960, KIDNE20191870, OCBF20174890, PLACE60073090, PLACE60181870, PROST20016760,
 PUAEN10000650, SKNMC20006350, SPLEN20017610, SPLEN20063250, SPLEN20126110, SPLEN20135030,
 TESTI20061200, TESTI20262150, THYMU10004280, THYMU20139160, TRACH20011010

[0294] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 39).
 15 BRAMY20001510, BRAMY20043630, BRAMY20204270, BRAMY20227860, CTONG20029030, CTONG20168460,
 CTONG20186290, FEBRA20039260, FEBRA20078800, FEBRA20163980, HCHON20000870, HLUNG20008460,
 HLUNG20009260, HLUNG20009550, HLUNG20010130, HLUNG20011260, HLUNG20011440, HLUNG20011460,
 HLUNG20012140, HLUNG20014590, HLUNG20015070, HLUNG20015180, HLUNG20020500, HLUNG20020850,
 HLUNG20021450, HLUNG20023030, HLUNG20024050, HLUNG20025620, HLUNG20028110, HLUNG20029420,
 20 HLUNG20029490, HLUNG20030420, HLUNG20030490, HLUNG20030610, HLUNG20031620, HLUNG20032460,
 HLUNG20033060, HLUNG20033310, HLUNG20033350, HLUNG20034970, HLUNG20037140, HLUNG20037160,
 HLUNG20037780, HLUNG20038330, HLUNG20041540, HLUNG20041590, HLUNG20042730, HLUNG20045340,
 HLUNG20047070, HLUNG20050760, HLUNG20051330, HLUNG20052300, HLUNG20054790, HLUNG20055240,
 HLUNG20056560, HLUNG20057380, HLUNG20059240, HLUNG20060670, HLUNG20063700, HLUNG20065700,
 25 HLUNG20065990, HLUNG20067810, HLUNG20068120, HLUNG20069350, HLUNG20070410, HLUNG20072100,
 HLUNG20072190, HLUNG20072450, HLUNG20074330, HLUNG20079310, HLUNG20081390, HLUNG20081530,
 HLUNG20082350, HLUNG20083330, HLUNG20083480, HLUNG20083840, HLUNG20083960, HLUNG20084790,
 HLUNG20085210, HLUNG20088750, HLUNG20092530, HLUNG20093030, HLUNG20094130, KIDNE20142900,
 PROST20016760, PROST20052850, SKNMC20006350, SMINT20035050, SPLEN20012450, TESTI20057590,
 30 TESTI20061200, TESTI20067480, TESTI20116050, THYMU10004280, THYMU20010180, THYMU20139160,
 TRACH20011010, UTERU20016580, UTERU20127030

[0295] These genes are involved in regeneration of tissues and/or cells.

EXAMPLE 8

35

Expression frequency analysis by PCR

[0296] Specific PCR primers were prepared based on the full-length nucleotide sequences, and the expression frequency was analyzed by the ATAC-PCR method (Adaptor-tagged competitive PCR method: Nucleic Acids Research
 40 1997, 25(22): 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds.,
 Muramatsu and Nawa (Shujunsha, 2000): 104-112). Inflammation-related genes can be identified by revealing the
 genes whose expression levels are altered depending on the presence of an inflammation-inducing factor. Then, by
 using THP-1 cell line, which is a cell line of monocyte line, and TNF- α , which is an inflammation-inducing factor, suitable
 for this system, the genes whose expression levels are altered depending on the presence of the factor were searched
 45 for by the system.

[0297] THP-1 cell line (purchased from DAINIPPON PHARMACEUTICAL) was cultured to be confluent in RPMI1640
 medium (sigma) containing 5% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium con-
 taining 10 ng/ml TNF- α (human recombinant TNF- α ; Pharmacia Biotech), and the culture was continued at 37°C under
 50 5% CO₂. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent
 (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent.
 In addition, total RNA was also extracted from the cells cultured without stimulation of TNF- α .

[0298] The genes involved in the onset of gastritis and gastroduodenal ulcer induced by the infection of *Helicobacter pylori* to the epithelia of stomach can be identified by revealing the genes whose expression levels are altered depending
 on co-culturing the cells with *Helicobacter pylori*. A recent study has suggested that various substances derived from
 55 *Helicobacter pylori* trigger the inflammation reaction. In particular, the members belonging to the family of genes called
 "cag pathogenicity island (cag PAI)" contribute to the activation of the NF- κ B pathway (Gastroenterology 2000, 119:
 97-108). Further, it has been found that cag PAI is involved in the onset of gastritis and the like by the study using an
 animal model (Journal of Experimental Medicine 2000, 192:1601-1610). Then, by using co-culture of a gastric cancer

cell line with cag PAI-positive *Helicobacter pylori* (TN2), suitable for this system, the genes whose expression levels are altered depending on the presence of *Helicobacter pylori* were searched for by the system. Further, in order to study the involvement of cag PAI in the alterations of gene expression levels depending on the co-culture with *Helicobacter pylori*, the altered expression levels were compared between the cells co-cultured with a strain of *Helicobacter pylori* (TN2ΔcagE strain) having a mutation in cagE, which is one of the cag PAI genes, and the cag PAI-positive strain (TN2).

[0299] A gastric cancer cell line MKN45 (provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research) was cultured to be confluent in RPMI1640 medium (sigma) containing 10% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 100-fold excess (in terms of the number of cells or the number of colonies) of *Helicobacter pylori* (cag PAI positive strain (TN2) and cagE mutant (TN2ΔcagE): both were provided by Prof. Omata, Faculty of Medicine, The University of Tokyo), as compared with the number of the cancer cells. The culture was continued at 37°C under 5% CO₂. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without *Helicobacter pylori*.

[0300] The analysis by the ATAC-PCR method was carried out basically according to "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement (Genome Science Series 1, Eds., Muramatsu and Nawa (Shunjunsha, 2000): 104-112). Adapter ligation to the internal standard sample (sample to make the calibration curve for the clone of interest) and test sample was carried out in the two separate reaction systems indicated below. The combination of 6 types of adapters (AD-1, AD-2, AD-3, AD-4, AD-5 and AD-6: see the sequences indicated below) and the samples are as follows.

Reaction system A

[0301]

AD1; internal standard, 10-fold
AD2; THP-1 cells, unstimulated
AD3; internal standard, 3-fold
AD4; THP-1 cells, TNF-α stimulation for one hour
AD5; THP-1 cells, TNF-α stimulation for three hours
AD6; internal standard, 1-fold
Reaction system B

AD1; internal standard, 1-fold
AD2; MKN45 cells, unstimulated
AD3; internal standard, 3-fold
AD4; MKN45 cells, co-cultured with TN2 (*Helicobacter pylori*)
AD5; internal standard, 10-fold
AD6; MKN45 cells, co-cultured with TN2ΔcagE (cagE gene mutant) Adapter sequences:

AD1 ;

SEQ ID NO: 3941//5'-GTACATATTGTCGTTAGAACGCG-3'

SEQ ID NO: 3942//3'-CATGTATAACAGCAATCTTGCGCCTAG-5'

AD2 ;

SEQ ID NO: 3943//5'-GTACATATTGTCGTTAGAACGCGACT-3'

SEQ ID NO: 3944//3'-CATGTATAACAGCAATCTTGCGCTGACTAG-5'

AD3 ;

SEQ ID NO: 3945//5'-GTACATATTGTCGTTAGAACGCGCATACT-3'

SEQ ID NO: 3946//3'-CATGTATAACAGCAATCTTGCGCGTATGACTAG-5'

AD4;

SEQ ID NO: 3947//5'-GTACATATTGTCGTTAGAACGCGATCCATACT-3'

SEQ ID NO: 3948//3'-CATGTATAACAGCAATCTTGCGCTAGGTATGACTAG-5'

AD5;

SEQ ID NO: 3949//5'-GTACATATTGTCGTTAGAACGCGTCAATCCATACT-3'

SEQ ID NO: 3950//3'-CATGTATAACAGCAATCTTGCGCAGTTAGGTATGACTAG-5'

AD6;

SEQ ID NO: 3951//5'-GTACATATTGTCGTTAGAACGCGTACTCAATCCATACT-3'

SEQ ID NO: 3952//3'-CATGTATAACAGCAATCTTGCGCATGAGTTAGGTATGACTAG-5'

[0302] The internal standard sample used for this assay was a mixture of total RNAs from tissues (or culture cells; all from UNITECH) of brain, kidney, NT2, testis, thymus, and trachea. RNA was prepared according to the standard method.

[0303] The sequences of primers specific to the genes and the names of clones of interest in the analysis are as follows. The gene specific primers were designed to produce the PCR products of 70 to 200 bp, which are derived from the adapter-containing cDNA. The sequence of adapter-specific primer (labeled with fluorescence (FAM)) used in the competitive PCR was GTACATATTGTCGTTAGAACGC (22 nucleotides; SEQ ID NO: 3953). PCR was basically carried out with a cycling profile of preheating at 94°C for 3 minutes, and 35 or 40 cycles of denaturation at 94°C for 30 seconds/annealing at 50°C for 60 seconds/extension at 72°C for 90 seconds.

The nucleotide sequences of clone specific primers used in the experiments

[0304] Clone name, primer sequence and SEQ ID NO are indicated below in this order. Each is demarcated by a double slash mark (/).

ADRG120036380//CTACTCAAGGACAGCCACAC//SEQ ID NO: 3954
 ASTRO20045840//GGATGTAGTGGGAAACAATG//SEQ ID NO: 3955
 ASTRO20055930//TGCTTTTCATTCTCCTTAGT//SEQ ID NO: 3956
 ASTRO20088950//TACGTGCTCATTCTTACTTGGT//SEQ ID NO: 3957
 BNGH420052350//GCCAGTTTCTTTATGATTGA//SEQ ID NO: 3958
 BRACE20052530//AATGACTTCGTTAGGATGCC//SEQ ID NO: 3959
 BRACE20054080//GCTGTTGACTTCATTGGA//SEQ ID NO: 3960
 BRAMY20003880//TTGGTACTTATTCTGAGGCA//SEQ ID NO: 3961
 BRAMY20027390//GATTTTAGTGAAACATGCCA//SEQ ID NO: 3962
 BRAMY20028530//TTAAAACTGAGGACATTCTG//SEQ ID NO: 3963
 BRAMY20035380//AGAGAAGGCAGTCTAGCTTA//SEQ ID NO: 3964
 BRAMY20036530//AGGGTATGGTAACTTCTGCA//SEQ ID NO: 3965
 BRAMY20050940//AAAGGAGGGACTAGAAACT//SEQ ID NO: 3966
 BRAMY20072440//ACTATGACGAGGGAACAAGA//SEQ ID NO: 3967

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BRAMY20096930//GAGGAGAACACAAGTATGGT//SEQ ID NO: 3968
 5 BRAMY20118410//AAGGTCACCTTCTAAACACAC//SEQ ID NO: 3969
 BRAMY20237190//GGAGTGATTTCAGGAGATGTG//SEQ ID NO: 3970
 BRAWH20055330//GCAACAGAGACTTTATTGGT//SEQ ID NO: 3971
 BRAWH20078620//GAGAGACTTATCACAGCCAT//SEQ ID NO: 3972
 10 BRAWH20190530//ATGGGATTCTGTGACTTCTC//SEQ ID NO: 3973
 BRCAN20001480//CAGCAACAGTAATGGGAATT//SEQ ID NO: 3974
 BRHIP10000720//AGGTTAGGATTTCTTTAGCA//SEQ ID NO: 3975
 15 BRHIP10001040//TACTTGGAGACAACAGGGAG//SEQ ID NO: 3976
 BRHIP20000210//GTGTTTGTGGGCATAGACAT//SEQ ID NO: 3977
 BRSSN20001970//AATGTATTTCAGTTCCTTTCC//SEQ ID NO: 3978
 BRSSN20091190//GTGTCATCACTAGCACCAAG//SEQ ID NO: 3979
 20 CD34C20001750//TGGACTTAGGGACCTGACTC//SEQ ID NO: 3980
 CTONG20078340//CTCTTTACCTAGTTTGGTCA//SEQ ID NO: 3981
 CTONG20079590//TACTTATTTTACAGGGGCC//SEQ ID NO: 3982
 25 CTONG20083980//CAGCATTTTCTATATAGCC//SEQ ID NO: 3983
 CTONG20085210//CCAGAAGAGTAGCAAGAATT//SEQ ID NO: 3984
 DFNES20063460//CTATTTTAACCCCTGCCCTC//SEQ ID NO: 3985
 30 DFNES20072990//GGAGGTATCTATTAGGGTGA//SEQ ID NO: 3986
 FCBBF20029280//GACTGAGATGAACTGGAAGA//SEQ ID NO: 3987
 FCBBF20032930//TCACAATACAGTCCCCTAGT//SEQ ID NO: 3988
 FCBBF20036360//ATTTGTATCACTTTGGTGCA//SEQ ID NO: 3989
 35 FCBBF30022680//CTCCAGAAAATGCATGAATC//SEQ ID NO: 3990
 FCBBF30078600//CTTCAACAGTGCTTTTCCTT//SEQ ID NO: 3991
 FCBBF30105080//CTGTGCACCCACTCTTTATT//SEQ ID NO: 3992
 40 FCBBF30169870//TCCAGTATTTTCCACTTTGA//SEQ ID NO: 3993
 FCBBF30225930//ACTATTTTATGGTCACGGCC//SEQ ID NO: 3994
 FCBBF50000610//AGTTAACGTATCTGGCAAAG//SEQ ID NO: 3995
 FEBRA20007820//GTTTCTCACTGTCCTGTTTT//SEQ ID NO: 3996
 45 FEBRA20031280//ACTATTTTATGGTCACGGCC//SEQ ID NO: 3997
 FEBRA20031810//TGCAATCATCTCTGTATCCC//SEQ ID NO: 3998
 FEBRA20039260//GTCAGAACCCACTTCACATC//SEQ ID NO: 3999
 50 FEBRA20046280//TCTCTGTCTGTGTCTAAG//SEQ ID NO: 4000
 FEBRA20084750//TTAGCATGTACTGGGAAAGC//SEQ ID NO: 4001
 FEBRA20182030//AAAACACAAAATGACACCCC//SEQ ID NO: 4002
 55 HLUNG20041540//AAAGTTCCTCTGCATTCACC//SEQ ID NO: 4003

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HLUNG20092530//TTTTTCATCCCAGAGTTATTA//SEQ ID NO: 4004
 KIDNE20084030//AGGGAATAACTTGCAGCTTG//SEQ ID NO: 4005
 5 KIDNE20084800//GTAATGTAGGGAGACTGCCG//SEQ ID NO: 4006
 KIDNE20134130//AATCCCCTCTTTTGTCTCAT//SEQ ID NO: 4007
 KIDNE20182540//ACAGATAGCCTGGATTGAAA//SEQ ID NO: 4008
 10 KIDNE20186170//TTGTATCTGAGCTGGGGTTT//SEQ ID NO: 4009
 KIDNE20188630//CCCTACATATCTCTACCCAT//SEQ ID NO: 4010
 LIVER20007750//TATTTAGAAACGCAGACCCC//SEQ ID NO: 4011
 15 MESAN20021220//TAGAAGTCAACAAAAGGCAC//SEQ ID NO: 4012
 MESAN20084150//TCCATAAGGCACAGATTTGA//SEQ ID NO: 4013
 NT2NE20059210//ATAATGACAATGCCAGTAGT//SEQ ID NO: 4014
 NT2NE20082130//TGAGGTACATCCAAATTAAA//SEQ ID NO: 4015
 20 NT2NE20092950//ATGATTACTCGGTTTCCAGA//SEQ ID NO: 4016
 NT2RP70031070//CAGTTAGTAGACAGACGGGG//SEQ ID NO: 4017
 OCBBF20012520//TCTGCCTGTAGTTGCCATTA//SEQ ID NO: 4018
 25 OCBBF20110210//AGGTGATAGGACTTTGTGCC//SEQ ID NO: 4019
 OCBBF20110730//TTAGATGCTCCCTAAGGTCC//SEQ ID NO: 4020
 OCBBF20155030//GCTAAAATCGTGCATCTGTA//SEQ ID NO: 4021
 30 OCBBF20165900//AGTTTTGTATCTCCTTGTC//SEQ ID NO: 4022
 OCBBF20170350//TAAGATGGAGTTCAGGGGAG//SEQ ID NO: 4023
 OCBBF20176650//GCACACAGGCAAATTCTAGT//SEQ ID NO: 4024
 PLACE60006300//TTCTGTAATAAGGGCTGTCA//SEQ ID NO: 4025
 35 PLACE60061370//TGTTCACAAATGGCATAAAA//SEQ ID NO: 4026
 PROST20011160//CTACTAACTCAACCACGCAT//SEQ ID NO: 4027
 PROST20041460//CCATTTACGTACCTCTCTG//SEQ ID NO: 4028
 40 PROST20065100//ACTATTTTATGGTCACGGCC//SEQ ID NO: 4029
 PROST20075280//ACGTTGACTCTGATAGCCTG//SEQ ID NO: 4030
 PROST20106060//AATTCTTTTGACATTGCTTG//SEQ ID NO: 4031
 45 PROST20110120//GATAAATTCAGCAAGAGCAT//SEQ ID NO: 4032
 SKMUS20091900//AACTCTGCACTCCATAACTG//SEQ ID NO: 4033
 SMINT20024140//AAGCCTCTAAAAGTCAACAC//SEQ ID NO: 4034
 SMINT20092160//TTAAACAAGTGAGCCTCAGA//SEQ ID NO: 4035
 50 SPLEN20040780//TTTCCTGTTTGGTTAGTTTT//SEQ ID NO: 4036
 SPLEN20110860//CTGACGGAAACTTCTAATT//SEQ ID NO: 4037
 SPLEN20177400//ATATCTGGTTGTTGGGTTTT//SEQ ID NO: 4038
 55 TESTI20038240//GTCTGTCTTGATGGATTGGA//SEQ ID NO: 4039

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5 TESTI20043130//AACTATCAGACTGCAAGAGC//SEQ ID NO: 4040
 TESTI20046540//GGTAGCCAATAGCAAACAGG//SEQ ID NO: 4041
 TESTI20047370//ACGTTGCATAATCCTCAGTC//SEQ ID NO: 4042
 TESTI20057200//AGTCCCAGTCTCTAGTTCGG//SEQ ID NO: 4043
 10 TESTI20057590//ACATTTTGGTATTGACACTT//SEQ ID NO: 4044
 TESTI20113940//GTCAGTCCACCTTACTCTTT//SEQ ID NO: 4045
 TESTI20149880//CAAACGATTACGACACAAAA//SEQ ID NO: 4046
 TESTI20151800//CGTTCCTCAGGTAGCAAGAT//SEQ ID NO: 4047
 15 TESTI20173050//ACATGGCTGAAGGTGATTTT//SEQ ID NO: 4048
 TESTI20198600//TTTAGAAACATTGGCATCAG//SEQ ID NO: 4049
 TESTI20257910//CTGCCTAGAGTAGAACAAAA//SEQ ID NO: 4050
 20 TESTI20262940//CTCCCAATCTCAAACACAAG//SEQ ID NO: 4051
 THYMU20046770//CTTCTGCCGAGTTTGTGTAA//SEQ ID NO: 4052
 THYMU20058550//GATGCTGAGAAGGTGTAGT//SEQ ID NO: 4053
 THYMU20062520//AGTCTCAGGATGGGTAAAGG//SEQ ID NO: 4054
 25 THYMU20062770//AGAGTTAAGAACCGAGGGAT//SEQ ID NO: 4055
 THYMU20078240//CAAGCCAGGGAGATAGACAT//SEQ ID NO: 4056
 THYMU20150190//TACTACAATGTGGGCTACGG//SEQ ID NO: 4057
 30 TRACH20125620//CCACATTGTAAACAGTCCTT//SEQ ID NO: 4058
 TRACH20149740//AGATACATTTTCCGTCAAGC//SEQ ID NO: 4059
 TRACH20190460//CCAGAAGAGTAGCAAGAATT//SEQ ID NO: 4060
 35 UTERU20045200//ATTCAACTAAAACAAAGCTG//SEQ ID NO: 4061
 UTERU20064120//ACCCAGAAAAGAGATGAGAA//SEQ ID NO: 4062
 UTERU20103200//CTGTTCTGGCAAATAAGAG//SEQ ID NO: 4063
 ADRGL20046760//ATGTGAAGGAATGATGTACT//SEQ ID NO: 4064
 40 ASTRO20055530//GAATAATGAAGGGGACCAGA//SEQ ID NO: 4065
 BRAMY20076130//CCTTTCATGTCTCAGTATTT//SEQ ID NO: 4066
 CTONG20170940//ATACGTCAGAGGACACATGC//SEQ ID NO: 4067
 45 FCBBF20033360//TCCGTAGCAGTAGAAACATC//SEQ ID NO: 4068
 FCBBF30257370//CAGGTATGCTTGGAGTTTCA//SEQ ID NO: 4069
 FCBBF50001650//CGTGATTAGGAAGGGACAGT//SEQ ID NO: 4070
 FEBRA20040290//CCCAAGAACGAAACAAAAC//SEQ ID NO: 4071
 50 FEBRA20063720//AATAATGCCACCTATAAAA//SEQ ID NO: 4072
 FEBRA20098040//GAGGGGAATTGTCTAGTACAC//SEQ ID NO: 4073
 FEBRA20108580//TCATTTTGTCTAGTGCCCAT//SEQ ID NO: 4074
 55 MESAN20021860//ACACATTCCCATCAATAGGT//SEQ ID NO: 4075

MESAN20067430//AGCTAAGGAGGTTTTTCACAT//SEQ ID NO: 4076
 5 NT2NE20045190//GGAATATGTTGGGCTAGTTA//SEQ ID NO: 4077
 PROST20016760//AACTTCATCCATTCCAAGT//SEQ ID NO: 4078
 SKNSH20007160//TTAAACCAACATTGAGGAAA//SEQ ID NO: 4079
 10 SMINT20006020//CTTGGTTGTCCCCTTTCTAG//SEQ ID NO: 4080
 TESTI20059370//GGCTGACTTTTCTCCTACAG//SEQ ID NO: 4081
 TESTI20103690//CCACTTTATTTCTCCTCCCT//SEQ ID NO: 4082
 TESTI20254480//GTGGACACAAGTTGCTTTAC//SEQ ID NO: 4083
 15 THYMU10004280//GAGAGTCTGCCTAGCTGTGT//SEQ ID NO: 4084
 THYMU20030460//GCCCATGTGAGTAGGTGTAG//SEQ ID NO: 4085
 TRACH20090060//AGGGCCAACTTAAATCTCTG//SEQ ID NO: 4086
 20 UTERU20041970//GATAAACCCCAAACATGAAA//SEQ ID NO: 4087
 BRAMY20125360//GACAGACTAAACGTTGAGC//SEQ ID NO: 4088
 OCBBF20142290//CCAAGGAGAGTCAGTGACAG//SEQ ID NO: 4089
 SKMUS20006790//TTCAAAGCAGAGACTCCCT//SEQ ID NO: 4090
 25 TESTI20030610//TGAAGTCAGTACCAGGCTTG//SEQ ID NO: 4091
 UTERU20026620//GAGATTCCTAGTGGTGGTT//SEQ ID NO: 4092

30 **[0305]** The result of expression frequency analysis is shown in Table 40. The clones not shown in the table contain clones whose expression levels could not be measured because the levels were too low or the sizes of the PCR products were different from the expected. It was confirmed that the expression levels of IL-8 gene used as a positive control gene were elevated.

35 **[0306]** The result obtained by the search for the genes whose expression levels were altered depending on the presence of TNF- α in culturing THP-1 cell, which is a human monocyte cell line, showed that the clones whose expression levels were elevated by twofold or more one or three hours after the stimulation (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were

40 ASTRO20055530, ASTRO20055930, ASTRO20088950, BRAMY20027390, BRAMY20076130, BRAMY20118410, BRAMY20125360, BRAMY20237190, BRCAN20001480, BRHIP10000720, CD34C20001750, CTONG20078340, CTONG20085210, DFNES20063460, FCBBF20029280, FCBBF20033360, FCBBF30078600, FEBRA20007820, FEBRA20031280, FEBRA20031810, FEBRA20040290, HLUNG20041540, HLUNG20092530, MESAN20021860, MESAN20067430, MESAN20084150, NT2NE20092950, NT2RP70031070, OCBBF20012520, OCBBF20142290, OCBBF20165900, OCBBF20170350, OCBBF20176650, PLACE60006300, PROST20011160, PROST20106060, SPLEN20040780, SPLEN20110860, SPLEN20177400, TESTI20030610, TESTI20043130, TESTI20059370, TESTI20254480, THYMU10004280, THYMU20030460, THYMU20062520, THYMU20078240, THYMU20150190,

45 TRACH20090060, TRACH20125620, UTERU20026620, UTERU20045200, UTERU20064120, UTERU20103200. **[0307]** On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more by the TNF- α stimulation (the clones whose expression levels were increased 1 or 3 hours after the stimulation were excluded) were

50 BNGH420052350, BRACE20052530, BRAMY20003880, CTONG20170940, FCBBF30022680, FCBBF30225930, FCBBF30257370, FEBRA20046280, KIDNE20084030, KIDNE20188630, NT2NE20082130, OCBBF20110210, PLACE60061370, PROST20041460, PROST20075280, PROST20110120, SMINT20006020, TESTI20046540, TESTI20057200, TESTI20113940, TESTI20257910, TESTI20262940, TRACH20149740.

[0308] These clones were thus revealed to be involved in the inflammation reaction induced by TNF- α .

55 **[0309]** The result obtained by the search for the genes whose expression levels were altered depending on co-culturing gastric cancer cell line MKN45 with cag PAI positive *Helicobacter pylori* (TN2), showed that the clones whose expression levels were elevated by twofold or more (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were

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BRAMY20028530, BRAMY20035380, OCBBF20170350, PROST20011160, SKMUS20091900, SPLEN20040780, THYMU20078240, TRACH20190460, UTERU20045200, UTERU20064120, ASTRO20055530, CTONG20170940, FEBRA20040290, MESAN20067430, PROST20016760, THYMU10004280, TRACH20090060, UTERU20041970, OCBBF20142290, TESTI20030610.

[0310] Of these clones, the expression levels of BRAMY20035380, SKMUS20091900, SPLEN20040780, UTERU20064120, CTONG20170940, OCBBF20142290, TESTI20030610 were not increased by the co-culture with the cagE mutant (TN2ΔcagE). There may be the possibility that the expression levels of the 7 clones are altered via the NF-κB pathway. Among them, the expression levels of OCBBF20142290, SPLEN20040780, TESTI20030610, UTERU20064120 were also increased when human monocyte cell line THP-1 was stimulated with TNF-α.

[0311] On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more in the presence of *Helicobacter pylori* were

ASTRO20088950, BRACE20052530, BRAMY20003880, BRAMY20027390, BRAMY20036530, BRAMY20118410, BRHIP20000210, FCBBF20032930, FCBBF30022680, FCBBF30169870, FEBRA20182030, KIDNE20182540, LIVER20007750, MESAN20021220, NT2NE20059210, NT2NE20082130, OCBBF20155030, PROST20065100, PROST20075280, SPLEN20110860, TESTI20057200, TESTI20113940, TESTI20149880, TESTI20151800, TESTI20198600, TESTI20257910, THYMU20046770, THYMU20058550, THYMU20150190, FCBBF20033360, FCBBF30257370, FEBRA20098040, SMINT20006020.

[0312] These clones are involved in gastritis or gastroduodenal ulcer.

Table 3

Clone ID	CD34C	D30ST	D60ST	D90ST
ASTRO20010290	0	55.437	0	0
BRAMY20036530	0	33.144	0	0
BRAMY20043630	0	0	0	13.575
BRAMY20089770	0	0	0	63.803
BRAMY20190550	0	0	0	31.089
CD34C20001750	100	0	0	0
FCBBF20066340	0	0	0	76.503
FEBRA20040290	0	0	0	14.912
HLUNG20015180	0	0	0	8.491
HLUNG20041590	0	0	0	18.349
HLUNG20052300	0	36.241	0	0
KIDNE20084040	0	0	0	65.916
MESAN20021860	0	0	0	56.046
MESAN20027240	0	0	0	33.731
NTONG20055200	0	0	0	19.731
PROST20016760	0	0	0	15.442
PUAEN10001640	0	34.074	0	0
SMINT20006020	0	7.702	0	9.021
SMINT20028840	0	68.605	0	0
SMINT20035050	0	9.417	0	11.029
SPLEN20181570	81.506	0	0	0
TESTI20064530	0	0	77.29	0
TESTI20210030	0	0	0	90.471
THYMU20029830	0	42.091	0	0
THYMU20139160	0	0	0	3.486
TRACH20051590	0	0	0	75.217

Table 4

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
ADRGL20023920	0	6.69	0	0

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Table 4 (continued)

	Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
	ASTR020009140	0	0	13.389	0
5	BNGH420077980	0	0	20.754	0
	BNGH420086030	0	0	0	13.322
	BRACE20062580	0	0	3.585	2.717
	BRACE20079370	0	0	9.312	14.111
10	BRACE20215410	0	0	27.196	0
	BRAMY20003540	0	0	3.208	4.861
	BRAMY20043630	0	0	2.408	0
	BRAMY20076130	0	0	6.601	0
	BRAMY20095080	0	0	25.606	0
15	BRAMY20227860	0	2.798	6.17	3.596
	BRAWH20082550	0	0	0	9.738
	BRHIP10001040	0	0	0	2.323
	BRSSN20005610	0	22.393	0	0
20	CTONG20027660	0	0	50.642	0
	CTONG20044230	0	0	50.642	0
	CTONG20066110	0	0	19.131	0
	CTONG20079590	0	14.297	29.102	0
	CTONG20084660	0	0	2.553	0
25	CTONG20133720	0	8.861	0	9.111
	CTONG20165750	0	9.056	0	0
	CTONG20188080	0	10.319	0	0
	FCBBF20023490	0	7.376	0	7.583
30	FCBBF20033360	0	0	5.015	0
	FCBBF20059660	0	0	0	66.235
	FCBBF20070950	0	0	15.367	0
	FCBBF30004340	0	0	0	8.778
	FCBBF30095410	0	79.235	0	0
35	FCBBF30125460	0	0	0	9.321
	FCBBF30179180	0	0	56.418	0
	FCBBF30236670	0	1.325	4.494	2.724
	FCBBF30257370	0	19.522	0	0
	FCBBF50000610	0	0	56.418	0
40	FCBBF50001650	0	0	0	22.181
	FEBRA20038330	0	16.124	0	0
	FEBRA20039260	0	7.162	2.43	0
	FEBRA20063720	0	12.258	0	0
45	FEBRA20090220	0	4.602	3.122	4.732
	FEBRA20150420	0	0	33.26	0
	HEART10001490	0	0	9.27	0
	HLUNG20032460	0	0	0	21.278
	HLUNG20041590	0	0	0	4.932
50	KIANE20089870	0	0	0	4.145
	MESAN20016270	0	0	39.208	0
	MESAN20021860	0	0	0	7.532
	MESAN20060430	0	0	24.385	0
55	MESAN20067430	0	0	0	9.568
	NT2NE20018740	0	0	0	100
	NT2NE20018890	0	0	0	100
	NT2NE20021860	0	0	0	100

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Table 4 (continued)

	Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
	NT2NE20026200	0	0	0.808	2.449
5	NT2NE20026510	0	0	0	100
	NT2NE20028700	0	0	0	22.223
	NT2NE20033150	0	0	0	50.133
	NT2NE20037050	0	0	0	100
10	NT2NE20038870	0	0	0	100
	NT2NE20039210	0	0	0	100
	NT2NE20042550	0	0	0	59.083
	NT2NE20045190	0	0	5.05	15.306
	NT2NE20047870	0	0	0	100
15	NT2NE20053230	0	0	0	100
	NT2NE20053950	0	20.953	0	21.544
	NT2NE20059210	0	0	0	100
	NT2NE20059680	0	0	0	100
20	NT2NE20060750	0	0	0	100
	NT2NE20061030	0	39.18	0	40.284
	NT2NE20062880	0	0	0	100
	NT2NE20064780	0	0	0	100
	NT2NE20066590	0	0	0	100
25	NT2NE20069580	0	0	0	59.083
	NT2NE20070520	0	0	0	100
	NT2NE20073650	0	0	0	100
	NT2NE20077250	0	0	0	100
30	NT2NE20077270	0	0	0	100
	NT2NE20077860	0	0	0	100
	NT2NE20079670	0	0	0	100
	NT2NE20080770	0	0	0	100
	NT2NE20082130	0	0	0	38.09
35	NT2NE20082600	0	0	0	66.235
	NT2NE20086070	0	0	0	100
	NT2NE20087270	0	0	0	100
	NT2NE20087850	0	0	0	100
40	NT2NE20088030	0	0	0	60.425
	NT2NE20092950	0	20.298	0	20.87
	NT2NE20095230	0	0	0	55.188
	NT2NE20104000	0	0	0	100
	NT2NE20107810	0	0	0	100
45	NT2NE20108420	0	0	0	45.407
	NT2NE20111190	0	0	0	61.289
	NT2NE20112210	0	0	0	26.669
	NT2NE20114850	0	0	0	100
	NT2NE20117580	0	0	0	100
50	NT2NE20119980	0	0	0	100
	NT2NE20123610	0	0	0	100
	NT2NE20124570	0	0	0	100
	NT2NE20126030	0	0	0	100
55	NT2NE20127900	0	0	16.514	25.025
	NT2NE20140130	0	0	0	100
	NT2NE20140280	0	0	0	100
	NT2NE20141040	0	0	0	36.013

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Table 4 (continued)

	Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
	NT2NE20145250	0	0	0	100
5	NT2NE20146510	0	0	0	100
	NT2NE20148690	0	0	0	67.567
	NT2NE20149500	0	0	0	100
	NT2NE20150610	0	0	0	100
10	NT2NE20152620	0	0	0	100
	NT2NE20153620	0	0	0	60.858
	NT2NE20155650	0	0	0	100
	NT2NE20157120	0	0	0	100
	NT2NE20165190	0	0	0	100
15	NT2NE20167660	0	0	0	100
	NT2NE20173970	0	0	0	100
	NT2NE20177210	0	0	0	43.734
	NT2NE20181760	0	0	0	100
	NT2NE20181800	0	0	0	46.215
20	NT2NE20184720	0	0	0	100
	NT2RI20016240	0	0	100	0
	NT2RI20021200	0	0	8.844	0
	NT2RI20033920	0	0	100	0
25	NT2RI20093010	0	0	100	0
	NT2RP70001120	0	32.573	0	0
	NT2RP70001730	0	15.462	0	0
	NT2RP70003110	0	24.333	0	0
30	NT2RP70012830	0	5.639	0	5.798
	NT2RP70022820	0	66.955	0	0
	NT2RP70027790	0	60.194	0	0
	NT2RP70029780	0	100	0	0
	NT2RP70030840	0	100	0	0
35	NT2RP70031070	0	100	0	0
	NT2RP70031340	0	100	0	0
	NT2RP70031480	0	100	0	0
	NT2RP70035110	0	23.442	0	0
40	NT2RP70046410	0	64.358	0	0
	NT2RP70049610	0	100	0	0
	NT2RP70056290	0	100	0	0
	NT2RP70056690	0	100	0	0
	NT2RP70057500	0	13.6	0	0
45	NT2RP70064570	0	60.194	0	0
	NT2RP70074800	0	100	0	0
	NT2RP70075300	0	6.726	0	0
	NT2RP70075800	0	100	0	0
	NT2RP70080150	0	100	0	0
50	NT2RP70084540	0	100	0	0
	NT2RP70087140	0	7.444	15.153	7.654
	NT2RP70090870	0	17.122	11.617	0
	OCBBF20001780	0	0	15.351	0
55	OCBBF20009820	84.348	0	0	0
	OCBBF20142290	0	0	0	14.577
	OCBBF20155030	0	49.439	0	0
	OCBBF20175360	0	0	0	20.881

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
OCBBF20177540	0	25.509	0	0
OCBBF20177910	0	0	23.505	0
PLACE60054820	0	0	20.089	0
PLACE60061370	0	18.07	0	0
PLACE60073090	0	10.617	0	0
PLACE60162100	0	0	0	37.629
PROST20011800	0	0	0	50.542
PROST20045700	0	0	0	44.59
PROST20078710	0	0	0	33.633
PROST20094000	0	0	18.34	0
PUAEN10000650	0	3.375	0	0
PUAEN10001640	0	5.216	3.539	0
SKNMC20006350	0	2.005	2.041	4.124
SMINT20016150	0	49.972	0	0
SMINT20030740	0	5.712	0	0
SMINT20035510	0	0	28.984	0
SMINT20039050	0	0	18.576	9.383
SMINT20047290	0	39.6	0	0
SPLEN20063250	0	8.081	8.225	8.309
SPLEN20117580	0	0	0	24.462
SPLEN20125230	0	0	21.559	0
TESTI20030610	0	0	0	12.205
TESTI20043910	0	0	0	45.963
TESTI20066280	0	0	0	30.676
TESTI20067480	0	8.861	0	0
TESTI20105130	0	0	0 0	2.5
TESTI20106170	0	13.104	0	0
TESTI20143180	0	0	62.741	0
TESTI20221790	0	0	39.167	0
TESTI20254090	0	0	0	19.063
TESTI20274960	0	0	38.685	0
THYMU10004280	0	3.573	0	0
THYMU20007020	0	0	71.017	0
THYMU20104480	0	0	29.694	0
THYMU20139160	0	1.822	0.618	0
TRACH20026640	0	0	7.476	0
UTERU10001060	0	0	19.967	0
UTERU20026620	0	10.41	0	10.703
UTERU20079240	0	0	0	19.734
UTERU20083020	0	7.182	0	0
UTERU20102260	0	0	0	23.706
UTERU20132620	0	48.06	0	0

Table 5

Clone ID	BEAST	TBAES
CTONG20070780	0	97.283
CTONG20084660	0	89.108
HLUNG20045340	0	85.362

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Table 5 (continued)

Clone ID	BEAST	TBAES
TESTI20047370	0	71.55

Table 6

Clone ID	CERVX	TCERX
SMINT20030740	0	65.795

Table 7

Clone ID	COLON	TCOLN
UTERU2004037	68.149	0

Table 8

Clone ID	NESOP	TESOP
HLUNG20015180	51.695	0
NESOP20004520	100	0
NESOP20005040	100	0
TESOP10000350	0	86.127
TESOP10001600	0	100
THYMU20071120	0	81.712

Table 9

Clone ID	KIDNE	TKIDN
ASTR020009140	19.518	0
ASTR020027330	0	30.903
ASTR020055930	0	36.981
BGGI120010750	4.532	0
BNGH420074600	0	11.358
BRACE20050870	0	15.884
BRACE20054480	29.719	0
BRACE20062580	2.613	0
BRACE20219360	59.494	0
BRAMY20003540	4.676	0
BRAMY20003880	16.882	41.527
BRAMY20043630	3.51	0
BRAMY20055760	0	65.196
BRAMY20125360	0	32.672
BRAMY20190550	0	19.772
BRAMY20204270	3.618	0
BRAMY20227860	0	4.255
BRAWH20014590	0	23.509
BRAWH20093070	0	14.759
BRHIP10001040	0	5.496
CTONG20033750	59.93	0
CTONG20039370	59.93	0
CTONG20045500	59.93	0

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Table 9 (continued)

	Clone ID	KIDNE	TKIDN
	CTONG20079590	0	17.392
5	FCBBF20023490	14.59	0
	FCBBF30004340	0	10.386
	FCBBF30106950	0	69.888
	FCBBF30115230	0	69.888
	FCBBF30169280	0	38.857
10	FCBBF30225930	0	50.898
	FCBBF30282020	0	53.714
	FEBRA20038330	0	6.538
	FEBRA20039260	7.084	0
15	FEBRA20040290	7.711	0
	FEBRA20082660	0	77.359
	FEBRA20121200	0	63.078
	FEBRA20170240	0	63.078
20	HEART10001490	20.269	0
	HLUNG20041590	4.744	0
	HLUNG20068120	11.84	0
	HLUNG20072450	3.599	0
	HLUNG20083480	0	15.004
25	HLUNG20083960	18.946	0
	KIDNE20011600	100	0
	KIDNE20016360	59.589	0
	KIDNE20024380	100	0
	KIDNE20027980	100	0
30	KIDNE20080690	5.861	0
	KIDNE20081170	100	0
	KIDNE20083150	100	0
	KIDNE20083620	100	0
35	KIDNE20084030	40.03	0
	KIDNE20084040	34.084	0
	KIDNE20084730	100	0
	KIDNE20084800	100	0
40	KIDNE20086490	87.61	0
	KIDNE20086660	47.013	0
	KIDNE20086970	100	0
	KIDNE20087880	28.683	0
	KIDNE20088240	100	0
45	KIDNE20089870	3.987	0
	KIDNE20091090	100	0
	KIDNE20094260	100	0
	KIDNE20094670	59.494	0
	KIDNE20095530	100	0
50	KIDNE20133460	100	0
	KIDNE20133880	100	0
	KIDNE20134130	65.363	0
	KIDNE20134890	100	0
55	KIDNE20137310	100	0
	KIDNE20138450	38.971	0
	KIDNE20140870	22.93	0
	KIDNE20141120	100	0

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Table 9 (continued)

	Clone ID	KIDNE	TKIDN
5	KIDNE20141700	100	0
	KIDNE20142680	100	0
	KIDNE20142680	100	0
	KIDNE20142900	31.732	0
	KIDNE20143200	100	0
10	KIDNE20147170	100	0
	KIDNE20148080	100	0
	KIDNE20149780	60.365	0
	KIDNE20150730	100	0
	KIDNE20152440	100	0
15	KIDNE20154330	100	0
	KIDNE20154830	100	0
	KIDNE20155980	100	0
	KIDNE20157100	100	0
	KIDNE20160360	100	0
20	KIDNE20160960	100	0
	KIDNE20163710	100	0
	KIDNE20165390	100	0
	KIDNE20169180	100	0
	KIDNE20170400	19.556	0
25	KIDNE20173150	100	0
	KIDNE20173430	36.673	0
	KIDNE20176030	100	0
	KIDNE20181670	100	0
	KIDNE20182540	100	0
30	KIDNE20186170	100	0
	KIDNE20188630	100	0
	KIDNE20189890	100	0
	KIDNE20189960	100	0
	KIDNE20191870	100	0
35	MESAN20038520	0	11.358
	MESAN20041380	0	53.625
	OCBBF20016390	0	23.211
	OCBBF20142290	0	8.623
	OCBBF20174890	32.241	0
40	PLACE60061370	0	21.981
	PLACE60073090	10.501	0
	PLACE60181870	49.921	0
	PROST20016760	3.992	9.82
	PUAEN10000650	6.676	0
45	SMINT20039050	0	11.102
	SMINT20089210	0	12.885
	SPLEN20017610	42.429	0
	SPLEN20024930	0	22.541
	SPLEN20057830	0	35
50	SPLEN20063250	3.996	0
	SPLEN20126110	50.05	0
	SPLEN20135030	31.695	0
	SPLEN20136700	0	39.807
	TESTI20070740	0	75.118
55			

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Table 9 (continued)

Clone ID	KIDNE	TKIDN
TESTI20262150	40.96	0
THYMU20009500	0	24.928
THYMU20019260	0	36.869
THYMU20157620	0	19.973
TKIDN10000620	0	100
TKIDN10001710	0	100
TKIDN10001920	0	36.869
TRACH20011010	10.647	0
UMVEN10001380	0	4.196

Table 10

Clone ID	LIVER	TLIVE
CTONG20069320	20.862	0
FCBBF30236670	3.257	0
FEBRA20038220	77.547	0
FEBRA20039260	8.806	0
KIDNE20087880	71.317	0
LIVER20006260	100	0
LIVER20007690	85.922	0
LIVER20007750	100	0
LIVER20010510	100	0
LIVER20010760	100	0
LIVER20010990	100	0
LIVER20011640	100	0
LIVER20013890	100	0
LIVER20026440	100	0
LIVER20030650	100	0
LIVER20032340	100	0
LIVER20038000	100	0
LIVER20040740	100	0
LIVER20055270	100	0
MESAN20027240	21.684	0
NT2RI20021200	16.028	0
SKMUS20006790	6.063	0
TESTI20035330	22.045	0
THYMU10004280	8.787	4.346
THYMU20029830	31.692	0

Table 11

Clone ID	HLUNG	TLUNG
HLUNG20052300	23.611	0
SMINT20035050	6.135	0
HLUNG20041590	10.207	0
PROST20016760	8.589	0
BRAMY20043630	15.102	0
HLUNG20015180	4.723	0
THYMU20139160	1.939	0

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Table 11 (continued)

	Clone ID	HLUNG	TLUNG
5	HLUNG20020850	67.488	0
	HLUNG20032460	44.037	0
	BRAMY20204270	7.785	0
	BRAMY20001510	5.948	0
	BRAMY20227860	1.488	0
10	CTONG20029030	28.504	0
	CTONG20168460	76.291	0
	CTONG20186290	61.67	0
	FEBRA20039260	7.62	0
	FEBRA20078800	33.686	0
15	FEBRA20163980	38.327	0
	HCHON20000870	23.288	0
	HLUNG20008460	67.54	0
	HLUNG20009260	100	0
	HLUNG20009550	100	0
20	HLUNG20010130	100	0
	HLUNG20011260	100	0
	HLUNG20011440	100	0
	HLUNG20011460	76.577	0
	HLUNG20012140	100	0
25	HLUNG20014590	36.045	0
	HLUNG20015070	17.804	0
	HLUNG20020500	100	0
	HLUNG20021450	68.006	0
	HLUNG20023030	100	0
30	HLUNG20024050	100	0
	HLUNG20025620	100	0
	HLUNG20028110	76.618	0
	HLUNG20029420	100	0
	HLUNG20029490	81.173	0
35	HLUNG20030420	100	0
	HLUNG20030490	100	0
	HLUNG20030610	100	0
	HLUNG20031620	80.237	0
	HLUNG20033060	36.529	0
40	HLUNG20033310	100	0
	HLUNG20033350	100	0
	HLUNG20034970	79.349	0
	HLUNG20037140	100	0
	HLUNG20037160	100	0
45	HLUNG20037780	44.761	0
	HLUNG20038330	100	0
	HLUNG20041540	100	0
	HLUNG20042730	100	0
	HLUNG20045340	7.67	0
50	HLUNG20047070	100	0
	HLUNG20050760	100	0
	HLUNG20051330	100	0
	HLUNG20054790	100	0
	HLUNG20055240	100	0

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Table 11 (continued)

Clone ID	HLUNG	TLUNG
HLUNG20056560	75.961	0
HLUNG20057380	100	0
HLUNG20059240	100	0
HLUNG20060670	100	0
HLUNG20063700	100	0
HLUNG20065700	62.8	0
HLUNG20065990	100	0
HLUNG20067810	100	0
HLUNG20068120	50.947	0
HLUNG20069350	100	0
HLUNG20070410	100	0
HLUNG20072100	54.241	0
HLUNG20072190	79.349	0
HLUNG20072450	7.744	0
HLUNG20074330	100	0
HLUNG20079310	100	0
HLUNG20081390	66.429	0
HLUNG20081530	100	0
HLUNG20082350	100	0
HLUNG20083330	100	0
HLUNG20083480	13.123	0
HLUNG20083840	100	0
HLUNG20083960	40.76	0
HLUNG20084790	100	0
HLUNG20085210	50.993	0
HLUNG20088750	100	0
HLUNG20092530	100	0
HLUNG20093030	100	0
HLUNG20094130	75.987	0
KIDNE20142900	68.268	0
PROST20052850	57.701	0
SKNMC20006350	2.134	0
SPLEN20012450	25.695	0
TESTI20057590	17.804	0
TESTI20061200	29.123	0
TESTI20067480	18.856	0
TESTI20116050	30.168	0
THYMU10004280	7.603	0
THYMU20010180	79.349	0
TRACH20011010	22.907	0
UTERU20016580	43.64	0
UTERU20127030	66.318	0

Table 12

Clone ID	NOVAR	TOVAR
KIDNE20089870	91.868	0
NT2RP70075300	76.633	0
TESTI20132310	94.177	0

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Table 13

Clone ID	STOMA	TSTOM
BNGH420087430	0	91.629
BRAMY20227860	1.35	0
BRAWH20027250	42.096	0
CTONG20174440	26.346	0
FEBRA20090220	4.442	0
PUAEN10000650	13.031	0
SMINT20023110	72.094	0
SMINT20030740	5.514	0
SMINT20045890	34.092	0
SPLEN20048800	2.011	0
SPLEN20139360	79.641	0
TESTI20063410	28.273	0
TESTI20150920	33.158	0
TRACH20026640	21.272	0
UTERU20041970	0	72.886

Table 14

Clone ID	UTERU	TUTER
ADRGL20020290	21.538	0
BRACE20038920	10.185	0
BRAMY20091230	39.224	0
BRAMY20093490	62.465	0
BRAMY20227860	2.268	0
BRHIP20005060	61.644	0
CTONG20069320	18.336	0
CTONG20083430	62.039	0
FCBBF30005360	41.409	0
FCBBF30257370	21.099	0
FEBRA20038330	5.808	0
FEBRA20039260	7.74	0
FEBRA20040260	43.146	0
FEBRA20078180	31.447	0
FEBRA20087550	10.505	0
HLUNG20015070	9.042	0
HLUNG20015180	7.196	0
MESAN20007110	50.674	0
MESAN20067430	20.114	0
MESAN20095800	14.162	0
NT2RP70057500	14.698	0
SKMUS20008730	2.775	0
SKNMC20006350	1.084	0
SMINT20035050	3.116	0
SMINT20045890	19.084	0
SPLEN20073880	30.142	0
SPLEN20076470	17.567	0
SPLEN20118050	33.583	0
TESTI20030610	12.829	0

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Table 14 (continued)

	Clone ID	UTERU	TUTER
	TESTI20035330	9.688	0
5	TESTI20057590	9.042	0
	TESTI20059080	9.096	0
	TESTI20105130	0	57.51
	THYMU10004280	3.861	0
10	THYMU20139160	1.969	21.546
	UTERU10001060	31.804	0
	UTERU10001870	100	0
	UTERU20000230	34.999	0
	UTERU20000950	3.88	0
15	UTERU20011760	100	0
	UTERU20013890	100	0
	UTERU20016580	22.164	0
	UTERU20026620	33.752	0
20	UTERU20027360	100	0
	UTERU20029930	72.842	0
	UTERU20031350	100	0
	UTERU20035770	100	0
	UTERU20040150	100	0
25	UTERU20040370	6.264	0
	UTERU20040390	100	0
	UTERU20040730	100	0
	UTERU20041630	100	0
30	UTERU20041970	6.578	0
	UTERU20045200	62.039	0
	UTERU20051790	100	0
	UTERU20064120	100	0
	UTERU20065470	50.58	0
35	UTERU20079240	20.742	0
	UTERU20083020	7.762	0
	UTERU20086530	100	0
	UTERU20087070	100	0
40	UTERU20087850	100	0
	UTERU20089300	27.655	0
	UTERU20089390	17.567	0
	UTERU20089620	100	0
	UTERU20090940	100	0
45	UTERU20091470	100	0
	UTERU20094830	100	0
	UTERU20095100	39.739	0
	UTERU20099040	100	0
	UTERU20099510	100	0
50	UTERU20101150	100	0
	UTERU20102260	24.918	0
	UTERU20103040	100	0
	UTERU20103200	51.815	0
55	UTERU20104310	100	0
	UTERU20106510	100	0
	UTERU20121140	100	0
	UTERU20122520	51.33	0

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Table 14 (continued)

Clone ID	UTERU	TUTER
UTERU20125810	100	0
UTERU20127030	33.682	0
UTERU20127150	62.412	0
UTERU20128560	36.129	0
UTERU20132620	51.94	0
UTERU20134830	100	0
UTERU20139760	100	0
UTERU20140010	100	0
UTERU20167570	100	0
UTERU20168960	100	0
UTERU20169020	100	0
UTERU20173030	100	0
UTERU20176230	72.842	0
UTERU20177150	100	0
UTERU20181270	100	0
UTERU20185220	100	0
UTERU20188670	100	0
UTERU20188840	40.303	0

Table 15

Clone ID	NTONG	CTONG
ADRGL20023920	13.989	0
BRACE20038920	0	24.929
BRACE20050870	0	34.54
BRACE20061620	63.015	0
BRAMY20036530	21.217	0
BRAMY20076130	0	6.434
BRAMY20204270	0	2.419
BRAMY20267780	0	4.633
BRCAN10001680	14.71	0
CTONG10000090	0	87.752
CTONG20000340	0	100
CTONG20002790	0	100
CTONG20004110	0	100
CTONG20004520	0	100
CTONG20007660	0	100
CTONG20008190	0	100
CTONG20008460	0	100
CTONG20015240	0	100
CTONG20017490	0	100
CTONG20020660	0	100
CTONG20020950	0	100
CTONG20027660	0	49.358
CTONG20029030	0	44.292
CTONG20030280	0	100
CTONG20031150	0	100
CTONG20031890	0	62.139
CTONG20032930	0	29.763

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Table 15 (continued)

	Clone ID	NTONG	CTONG
5	CTONG20033500	0	100
	CTONG20033610	0	57.263
	CTONG20033750	0	40.07
	CTONG20035240	0	55.786
	CTONG20036800	0	100
10	CTONG20036990	0	100
	CTONG20039370	0	40.07
	CTONG20041150	0	100
	CTONG20041260	0	100
	CTONG20042640	0	100
15	CTONG20044230	0	49.358
	CTONG20044870	0	74.685
	CTONG20045500	0	40.07
	CTONG20046690	0	100
	CTONG20049480	0	100
20	CTONG20050490	0	100
	CTONG20051100	0	100
	CTONG20051450	0	100
	CTONG20052780	0	100
	CTONG20053990	0	100
25	CTONG20055670	0	100
	CTONG20055850	0	24.814
	CTONG20056150	0	51.203
	CTONG20057750	0	100
	CTONG20057950	0	54.423
30	CTONG20059130	0	72.445
	CTONG20060040	0	72.825
	CTONG20061290	0	100
	CTONG20062730	0	100
	CTONG20063770	0	62.139
35	CTONG20063930	0	28.37
	CTONG20065240	0	100
	CTONG20065680	0	100
	CTONG20066110	0	37.292
	CTONG20068360	0	100
40	CTONG20069320	0	11.22
	CTONG20069420	0	42.813
	CTONG20070090	0	100
	CTONG20070720	0	7.689
	CTONG20070780	0	2.717
45	CTONG24070910	0	100
	CTONG20071040	0	32.374
	CTONG20071680	0	49.582
	CTONG20072930	0	100
	CTONG20073990	0	100
50	CTONG20074000	0	100
	CTONG20074170	0	55.786
	CTONG20074740	0	100
	CTONG20076230	0	100
	CTONG20076810	0	100
55			

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Table 15 (continued)

	Clone ID	NTONG	CTONG
	CTONG20077760	0	100
5	CTONG20078340	0	74.685
	CTONG20079590	0	9.455
	CTONG20080140	0	27.673
	CTONG20081840	0	100
10	CTONG20083430	0	37.961
	CTONG20083980	0	100
	CTONG20084020	0	100
	CTONG20084660	0	2.488
	CTONG20085210	0	27.762
15	CTONG20133720	18.528	46.879
	CTONG20165590	0	100
	CTONG20165750	0	11.978
	CTONG20166580	0	100
20	CTONG20167750	0	100
	CTONG20168240	37.367	11.818
	CTONG20168460	0	23.709
	CTONG20169040	0	100
	CTONG20169530	0	100
25	CTONG20170940	0	89.253
	CTONG20174290	0	100
	CTONG20174580	0	100
	CTONG20176040	0	100
30	CTONG20179390	0	100
	CTONG20179890	0	100
	CTONG20179980	0	100
	CTONG20180620	0	100
	CTONG20180690	0	100
35	CTONG20181350	0	100
	CTONG20183430	0	55.786
	CTONG20183830	0	22.718
	CTONG20184130	0	100
	CTONG20184830	0	100
40	CTONG20186140	0	100
	CTONG20186290	0	38.33
	CTONG20186370	0	39.387
	CTONG20186520	0	100
45	CTONG20186550	0	100
	CTONG20188080	43.151	6.824
	CTONG20189000	0	100
	CTONG20190290	0	100
	CTONG20190630	0	100
50	FCBBF20070950	0	14.977
	FCBBF30001100	0	24.477
	FCBBF30175350	32.34	10.228
	FCBBF40005000	0	20.766
55	FEBRA20027070	26.269	0
	FEBRA20038330	0	3.554
	FEBRA20039260	7.487	0
	FEBRA20040290	0	2.578

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Table 15 (continued)

Clone ID	NTONG	CTONG
FEBRA20046200	0	16.309
FEBRA20063720	0	8.106
FEBRA20078800	0	10.469
FEBRA20090220	0	12.173
HCHON20000870	0	7.237
HLUNG20068120	25.03	0
MESAN20008150	0	38.598
MESAN20027900	0	17.599
NT2NE20153620	0	39.142
NT2RP70001730	0	4.09
NT2RP70012830	0	3.729
NT2RP70027790	0	39.806
NT2RP70057500	0	8.993
NT2RP70064570	0	39.806
NT2RP70090870	35.801	0
NTONG20002230	50.815	0
NTONG20005310	100	0
NTONG20017620	29.697	0
NTONG20029850	100	0
NTONG20031580	100	0
NTONG20032100	100	0
NTONG20034540	67.622	0
NTONG20035150	80.903	0
NTONG20043080	100	0
NTONG'20048440	100	0
NTONG20049180	63.818	20.184
NTONG20053630	100	0
NTONG20053730	100	0
NTONG20053910	100	0
NTONG20055200	10.784	3.411
NTONG20058010	100	0
NTONG20058220	100	0
OCBBF20110730	0	11.1
OCBBF20177540	0	16.869
OCBBF20177910	0	22.909
PROST20016760	0	2.669
PROST20042700	0	33.088
PROST20050390	0	30.175
PROST20063430	50.958	0
PROST20130320	0	11.979
PUAEN10000650	7.056	0
PUAEN10001640	0	13.798
PUAEN20003120	0	19.799
SKMUS20006790	5.155	0
SKNMC20006350	0	3.316
SKNSH20007160	0	9.506
SMINT20030740	0	5.666
SMINT20035510	0	28.25
SMINT20089210	0	7.005
SPLEN20024930	0	12.254

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Table 15 (continued)

Clone ID	NTONG	CTONG
SPLEN20040780	0	20.5
SPLEN20063250	0	8.016
SPLEN20181570	0	4.523
SPLEN20187490	0	23.141
TESTI20047370	0	1.998
TESTI20057880	0	15.357
TESTI20064530	0	10.734
TESTI20079980	0	8.166
TESTI20105130	0	4.825
TESTI20118460	63.366	0
TESTI20121040	0	17.698
TESTI20197290	0	62.139
THYMU10004280	0	2.363
THYMU20030460	14.321	4.53
THYMU20055460	0	10.818
THYHN20089900	0	37.939
THYMU20121040	0	54.423
THYMU20139160	1.905	4.82
THYMU20145990	0	37.385
TRACH20011010	0	28.476
TRACH20090060	0	6.234
UTERU20000230	0	21.416
UTERU20000950	0	2.374
UTERU20016580	0	13.562
UTERU20045200	0	37.961
UTERU20083020	15.017	0

Table 16

Clone ID	IFCBF	IFBRA	OCBBF	BRACE	BRALZ	IBRAWY	IBRAWH	IBRCAN	IBRCOC	IBRHIP	IBRSSN	IBRSYN	IBRTHA
ADRL20020290	0	0	0	0	0	12.942	0	0	0	0	0	0	0
ADRL20021910	0	0	0	0	0	21.897	0	0	0	22.674	0	0	0
ADRL20023920	0	0	0	4.505	0	0	0	0	0	0	0	0	0
ADRL20046760	8.812	35.914	0	0	0	0	0	0	0	0	0	0	0
ADRL20062330	0	0	0	0	0	0	0	28.364	0	0	0	0	0
ADRL20079060	0	0	0	0	0	0	0	28.364	0	0	0	0	0
ASTR020009140	0	0	0	0	0	0	21.998	0	0	0	0	0	0
ASTR020020240	0	0	0	0	0	38.79	0	0	0	0	0	0	0
ASTR020027330	0	0	25.981	0	0	0	0	0	0	17.083	0	0	0
ASTR020047510	0	0	0	0	0	0	0	0	0	0	0	49.891	0
ASTR020055530	0	10.089	28.982	0	0	9.201	0	0	0	0	0	0	0
ASTR020055570	0	0	0	0	0	0	0	38.844	0	0	0	0	0
ASTR020055930	31.867	0	0	0	0	0	0	0	0	0	0	0	0
ASTR020090680	0	0	0	0	0	0	0	0	0	0	33.707	0	0
BGG1120010750	4.804	0	0	0	0	0	0	0	0	0	0	0	0
BNGH420021680	0	0	0	10.084	0	0	0	0	0	0	0	0	0
BNGH420023870	0	0	0	0	0	0	0	0	0	0	0	0	0
BNGH420059680	8.889	0	0	0	0	0	0	0	0	0	0	0	52.181
BNGH420074600	4.894	0	0	0	0	12.127	0	0	0	0	0	0	0
BNGH420085030	0	0	0	0	0	8.414	0	8.433	0	0	0	0	0
BRACE10000510	0	0	0	55.676	0	0	30.722	0	0	0	0	0	0
BRACE20003310	0	0	0	29.513	0	0	48.856	0	0	0	0	0	0
BRACE20007330	0	0	0	38.94	0	0	0	0	0	0	61.06	0	0
BRACE20009050	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20014450	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20017790	43.768	0	0	56.232	0	0	0	0	0	0	0	0	0
BRACE20018810	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20025820	0	0	0	50.035	0	0	0	0	0	49.965	0	0	0
BRACE20033920	0	20.132	9.638	6.346	0	12.24	0	0	0	0	0	0	0
BRACE20050870	6.844	0	26.708	8.793	0	0	0	0	0	0	0	0	0
BRACE20051600	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20051930	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20052430	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20052530	0	0	0	19.237	0	0	0	0	0	0	0	0	80.763
BRACE20054080	0	0	0	26.402	0	0	0	25.519	0	26.365	0	0	0
BRACE20054480	0	0	0	40.468	0	0	0	0	0	0	0	0	0

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Table 18

5	BRANY20003540	4.956	0	0	0	3.184	0	3.07	10.541	6.155	0	9.538	0	4.824	0
	BRANY20003880	0	0	0	0	0	0	11.085	19.028	0	0	11.478	0	0	0
	BRANY20005080	0	0	0	0	0	0	19.453	33.393	0	0	0	0	30.564	0
	BRANY20013670	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20016780	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20020440	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20021580	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20023390	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20023640	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20024790	0	0	0	0	0	0	38.893	0	0	0	0	0	61.107	0
	BRANY20027390	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20027990	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20028530	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20028620	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20033380	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20035830	9.114	0	0	0	0	0	22.586	0	0	0	0	0	0	0
	BRANY20036530	0	0	0	0	0	0	13.18	0	0	0	0	0	0	0
	BRANY20036610	0	0	0	0	0	0	61.711	0	0	0	0	0	0	0
	BRANY20038980	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20039290	61.747	0	0	0	0	0	38.233	0	0	0	0	0	0	0
	BRANY20040580	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20043520	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20043630	1.86	0	3.629	0	0	0	2.304	0	0	0	0	0	0	0
	BRANY20044920	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20045210	0	0	0	0	0	0	29.335	0	0	0	0	0	0	0
	BRANY20045420	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20047560	0	0	0	0	0	0	24.533	0	0	0	0	0	0	0
	BRANY20050640	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20050940	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20051820	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20052440	0	0	0	0	0	0	53.973	0	0	0	0	0	0	0
	BRANY20053910	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20055760	0	0	0	0	0	0	34.804	0	0	0	0	0	0	0
	BRANY20056620	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20056840	0	0	0	0	0	0	100	0	0	0	0	0	0	0
	BRANY20063750	0	0	0	0	0	0	53.973	0	0	0	0	0	0	0
	BRANY20072440	0	17.768	0	0	16.803	0	32.409	0	16.241	0	16.78	0	0	0

Table 19

[illegible]

[illegible]

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Table 22

[illegible]

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Table 24

[illegible]

Table 25

[illegible]

Table 26

[illegible]

Table 27

[illegible]

Table 28

[illegible]

Table 29

FEBRA20150420	0	34.905	0	0	0	31.834	0	0	0	0	0	0	0
FEBRA20151750	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20163980	9.44	12.825	0	0	0	0	0	0	0	0	0	0	0
FEBRA20170240	0	36.922	0	0	0	0	0	0	0	0	0	0	0
FEBRA20172230	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20173330	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20175020	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20175330	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20177800	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20180510	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20182030	42.399	57.601	0	0	0	0	0	0	0	0	0	0	0
FEBRA20187460	0	100	0	0	0	0	0	0	0	0	0	0	0
FEBRA20191720	0	100	0	0	0	0	0	0	0	0	0	0	0
HCHON2002650	0	0	0	19.66	0	0	0	0	0	0	0	0	0
HCHON2002710	13.027	17.697	0	0	0	0	0	0	0	0	0	0	0
HEART10001490	3.58	0	6.986	0	0	0	0	0	0	0	0	0	0
HLUNG20008460	0	0	32.46	0	0	0	0	0	0	0	0	0	0
HLUNG20011460	0	0	0	0	0	0	0	23.423	0	0	0	0	0
HLUNG20014590	0	0	0	0	0	0	0	11.025	0	0	0	0	0
HLUNG20015070	0	0	0	0	0	5.433	0	8.409	0	0	0	0	0
HLUNG20015180	0	3.161	0	0	0	0	0	0	0	0	4.688	0	0
HLUNG20020850	0	0	0	32.512	0	0	0	0	0	0	0	0	0
HLUNG20028110	0	0	0	0	0	23.382	0	0	0	0	0	0	0
HLUNG20031620	19.763	0	0	0	0	0	0	0	0	0	0	0	0
HLUNG20032460	0	0	0	21.215	0	0	0	13.47	0	0	0	0	0
HLUNG20033060	0	0	17.556	0	0	0	0	0	0	11.544	0	0	0
HLUNG20041590	2.514	3.415	0	0	0	3.115	0	3.122	0	0	0	0	0
HLUNG20045340	0	0	0	0	0	0	0	0	0	2.424	0	0	0
HLUNG20056560	0	0	24.039	0	0	0	0	0	0	0	0	0	0
HLUNG20068120	6.274	0	0	0	0	0	0	0	0	0	0	0	0
HLUNG20081390	0	0	0	0	0	0	0	0	0	0	0	0	0
HLUNG20083480	3.232	0	12.614	4.153	0	4.005	0	0	6.198	4.147	0	0	0
HLUNG20085210	0	0	0	0	0	0	0	0	0	0	0	24.45	0
HLUNG20094130	0	0	0	0	0	0	0	0	0	24.013	0	0	0
KTDNE20080690	0	0	0	7.981	24.298	11.545	0	3.857	17.867	3.985	12.514	12.092	0
KTDNE20084030	0	0	0	0	0	26.283	0	0	0	13.608	0	0	0
KTDNE20086660	0	0	0	0	0	0	52.987	0	0	0	0	0	0

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Table 33

[illegible]

Table 34

SPLN20024930	0	0	0	24.956	0	0	0	0	0	0	12.461	0	0	0	0
SPLN20040780	32.496	0	31.704	0	0	0	0	0	0	0	0	0	0	0	0
SPLN20048800	0	0	0	0	0	0	0	0	0.678	0	0	0	0	0	0
SPLN20055600	0	0	0	0	0	0	0	0	0	67.066	0	0	0	0	0
SPLN20057830	0	0	0	0	0	0	32.073	18.727	0	0	0	0	0	0	0
SPLN20063250	0	0	0	0	0	0	0	0	0	0	0	4.267	0	0	0
SPLN20071820	0	0	0	0	0	0	0	0	0	0	0	37.578	0	0	0
SPLN20073880	0	0	0	0	0	0	0	0	0	28.031	0	0	0	0	0
SPLN20076470	8.519	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SPLN20104690	0	0	0	0	0	0	0	0	56.874	0	0	0	0	0	0
SPLN20114190	0	0	0	0	0	0	0	0	0	0	57.672	0	0	0	0
SPLN20125230	0	0	0	21.397	0	0	0	0	41.362	0	0	0	0	0	0
SPLN20135030	0	0	0	0	0	0	0	0	20.858	0	0	0	0	0	0
SPLN20136700	0	0	0	22.036	0	0	0	0	0	0	22.006	0	0	0	0
SPLN20175920	0	0	0	57.706	0	0	0	0	0	0	0	0	0	0	0
SPLN20181570	3.585	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SPLN20183020	0	0	0	0	0	0	0	0	0	0	21.246	0	0	0	0
SPLN20187490	0	0	0	0	0	0	0	0	22.776	0	0	0	0	0	0
SPLN20193490	0	0	0	0	0	0	0	0	0	0	57.672	0	0	0	0
SPLN20193790	0	0	0	0	0	0	0	0	0	0	0	0	0	10.329	0
SPLN20197740	0	0	0	0	0	0	0	0	0	0	0	33.067	0	0	0
SPLN20200070	0	0	0	67.502	0	0	0	0	0	0	0	0	0	0	0
SPLN20200340	0	0	0	40.827	0	0	0	0	0	0	0	0	0	0	0
TESOP1000350	0	0	0	0	0	0	0	0	2.374	0	0	0	3.721	0	0
TEST120005980	0	0	0	28.345	0	0	0	0	0	0	0	0	0	0	0
TEST120030440	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEST120030610	0	0	0	0	0	0	7.709	0	7.726	0	0	0	0	0	0
TEST120031410	0	0	0	0	0	0	19.238	0	0	0	0	0	15.113	0	0
TEST120035330	4.698	0	0	0	0	0	5.821	0	5.835	0	0	0	0	25.343	0
TEST120047370	0	0	0	0	0	0	0	0	0	3.037	0	0	0	0	0
TEST120050400	56.537	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEST120050720	0	0	0	6.04	0	0	0	0	0	0	0	0	0	0	0
TEST120053780	56.537	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TEST120057430	0	0	0	5.84	0	0	0	0	5.644	0	0	0	0	0	0
TEST120057590	0	0	0	0	0	0	5.433	0	0	8.409	0	0	0	0	0
TEST120057840	0	0	0	0	0	0	0	0	61.764	0	0	0	0	0	0
TEST120057880	0	0	0	15.638	0	0	0	0	0	0	0	0	0	0	0

Table 35

5	TEST120059080	0	5.993	0	0	25.882	0	8.888	0	5.478	8.458	0	0	0	0	0	0
10	TEST120061200	0	9.745	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	TEST120062580	0	0	0	0	0	0	0	31.15	0	28.084	0	29.506	0	0	0	0
20	TEST120063410	0	0	0	0	9.861	0	9.51	0	0	14.718	9.848	0	0	0	0	0
25	TEST120064530	0	0	0	0	0	0	2.635	0	0	0	5.458	0	0	0	0	0
30	TEST120066280	0	0	0	0	0	0	0	33.259	0	0	0	0	0	0	0	0
35	TEST120067480	9.289	6.31	0	11.934	0	0	0	0	5.768	0	0	0	0	0	0	0
40	TEST120071630	0	0	0	62.564	0	0	0	0	0	0	0	0	0	0	0	0
45	TEST120079980	6.472	8.793	6.314	0	0	0	4.009	6.883	12.056	0	4.152	0	0	0	0	0
50	TEST120081890	0	63.862	0	0	0	0	61.711	0	0	0	0	0	0	0	0	0
55	TEST120089290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	TEST120090180	0	0	0	21.786	0	0	0	0	0	0	0	0	0	0	0	0
	TEST120105130	2.549	0	2.487	0	4.986	0	0	0	1.583	0	1.635	0	0	0	0	0
	TEST120106170	0	18.661	13.402	0	0	0	8.51	14.608	0	0	26.436	0	0	0	0	0
	TEST120121040	0	0	0	18.021	0	0	0	0	0	0	0	18.135	0	0	0	0
	TEST120150920	0	0	0	0	17.606	0	0	0	0	17.261	0	0	0	0	0	0
	TEST120169500	17.008	0	0	0	0	0	0	0	0	0	62.532	0	0	0	0	0
	TEST120193080	0	0	0	0	0	0	0	0	0	0	0	0	71.689	0	0	0
	TEST120215310	0	0	0	0	0	0	0	0	37.573	0	0	0	0	0	0	0
	TEST120221790	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	TEST120245860	0	0	0	62.554	0	0	0	0	0	0	0	0	0	0	0	0
	TEST120252690	0	33.792	0	0	0	0	0	0	24.136	18.635	0	0	0	0	0	0
	TEST120254090	0	0	0	0	0	0	12.041	0	0	0	0	0	0	0	0	0
	TEST120261160	0	0	0	0	0	0	0	0	35	0	0	0	0	0	0	0
	TEST120262150	0	0	42.353	0	0	0	0	0	0	0	0	0	0	0	0	0
	TEST120274960	0	0	0	0	0	0	0	0	0	0	38.341	0	0	0	0	0
	THYMU20007750	0	0	0	29.606	0	0	0	0	0	0	0	0	0	0	0	0
	THYMU20009460	0	16.274	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	THYMU20009710	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.62	0
	THYMU20019260	15.885	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	THYMU20028410	13.579	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	THYMU20030460	0	0	0	4.612	0	0	16.825	0	0	30.461	0	0	0	0	0	0
	THYMU20031330	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	THYMU20043440	0	0	0	0	0	0	29.394	0	0	0	0	0	0	0	0	0
	THYMU20044100	0	0	0	28.394	0	0	0	0	27.444	0	0	0	0	0	0	0
	THYMU20044520	0	28.639	0	0	0	0	26.302	0	0	0	0	0	0	0	0	0
	THYMU20049060	0	0	0	0	0	0	0	0	0	64.474	0	0	0	0	0	0

Table 36

THYMU20055460	5.716	0	5.577	0	54.873	0	0	0	0	0	0	3.667	0	11.127	0
THYMU20055740	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
THYMU20071120	3.627	0	3.539	0	0	0	0	0	0	0	0	0	0	0	0
THYMU20078020	0	56.251	0	0	0	0	0	0	0	0	0	0	0	0	0
THYMU20089900	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
THYMU20091040	0	0	0	0	0	0	0	0	0	0	0	0	0	30.29	0
THYMU20104480	0	0	22.379	0	0	0	0	0	0	0	0	0	0	20.408	0
THYMU20120240	7.548	0	0	0	0	0	0	0	0	0	0	0	0	0	0
THYMU20139160	1.433	0.649	0.932	1.841	1.868	2.958	2.031	2.965	3.663	2.451	0	0	0	0	0
THYMU20143230	0	0	0	0	0	53.973	0	0	0	0	0	0	0	0	0
THYMU20150190	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
THYMU20157620	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
THYMU20176010	48.624	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TKIDN10001920	15.885	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TRACH20012490	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TRACH20021000	0	14.835	0	0	0	8.484	0	0	0	0	0	0	0	0	0
TRACH20026640	0	0	0	7.419	0	0	0	0	0	0	0	0	0	0	0
TRACH20058000	0	0	0	0	0	23.543	0	0	0	0	0	0	0	0	0
TRACH20090060	0	0	0	0	0	6.122	0	0	0	0	0	0	0	0	0
TRACH20159390	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UWVEN10001380	0	0	3.528	0	0	0	0	0	0	0	0	0	0	0	0
UTERU10001060	15.424	0	0	0	0	0	0	32.805	0	0	0	0	0	0	0
UTERU20000230	0	0	0	21.808	0	0	0	0	0	0	0	21.777	0	0	0
UTERU20000950	1.882	2.557	0	2.418	0	2.332	4.002	0	0	0	0	4.829	0	0	0
UTERU20026620	5.456	7.413	10.647	0	0	0	0	0	0	0	0	0	0	0	0
UTERU20041970	0	0	3.112	0	0	3.953	0	0	0	0	0	0	0	0	0
UTERU20065470	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UTERU20079240	0	0	0	0	19.675	0	0	0	0	0	0	0	0	49.42	0
UTERU20083020	0	0	0	0	0	4.664	8.006	4.675	7.218	4.83	0	0	0	20.266	19.583
UTERU20089300	0	0	0	0	0	0	0	0	0	0	0	0	0	7.328	0
UTERU20089390	8.519	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UTERU20095100	19.272	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UTERU20102260	0	0	0	15.526	0	0	0	0	0	0	0	0	0	0	0
UTERU20103200	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UTERU20127150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UTERU20128560	0	0	0	11.256	0	0	0	0	0	0	0	0	0	0	0

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Table 37

	Clone ID	FEHRT	HEART
5	BRAMY20043630	0	7.465
	BRAMY20072870	0	76.411
	BRAMY20227860	0	2.943
	BRAWH20093070	0	25.522
10	BRCAN10001680	0	14.799
	FCBBF30053300	86.185	0
	FEBRA20078800	0	33.301
	FEBRA20090220	0	9.681
	HCHON20000870	0	23.022
15	HEART10001420	0	100
	HEART10001490	0	14.37
	HEART20009590	0	100
	HEART20019310	0	100
	HEART20022200	0	100
20	HEART20031680	0	100
	HEART20047640	0	100
	HEART20063100	0	100
	HEART20082570	0	100
25	HLUNG20083960	0	40.294
	PLACE60088240	0	67.95
	PLACE60120280	0	50.712
	PROST20016760	0	8.491
	PROST20035170	0	23.745
30	PROST20062820	0	67.646
	PROST20127450	0	48.135
	SKMUS20006790	0	5.186
	SKMUS20008730	0	27.003
35	TESTI20270130	0	83.925

Table 38

	Clone ID	FEKID	KIDNE
40	ASTR020009140	0	19.518
	BGGI120010750	0	4.532
	BRACE20054480	0	29.719
	BRACE20062580	0	2.613
45	BRACE20219360	0	59.494
	BRAMY20001510	68.103	0
	BRAMY20003540	0	4.676
	BRAMY20003880	0	16.882
50	BRAMY20043630	0	3.51
	BRAMY20204270	0	3.618
	CTONG20033750	0	59.93
	CTONG20039370	0	59.93
	CTONG20045500	0	59.93
55	FCBBF20023490	0	14.59
	FEBRA20039260	0	7.084
	FEBRA20040290	0	7.711

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Table 38 (continued)

	Clone ID	FEKID	KIDNE
5	HEART10001490	0	20.269
	HLUNG20041590	0	4.744
	HLUNG20068120	0	11.84
	HLUNG20072450	88.657	3.599
	HLUNG20083960	0	18.946
10	KIDNE20011600	0	100
	KIDNE200163	0	59.589
	KIDNE20024380	0	100
	KIDNE20027980	0	100
	KIDNE20080690	0	5.861
15	KIDNE20081170	0	100
	KIDNE20083150	0	100
	KIDNE20083620	0	100
	KIDNE20084030	0	40.03
20	KIDNE20084040	0	34.084
	KIDNE20084730	0	100
	KIDNE20084800	0	100
	KIDNE20086490	0	87.61
	KIDNE20086660	0	47.013
25	KIDNE20086970	0	100
	KIDNE20087880	0	28.683
	KIDNE20088240	0	100
	KIDNE20089870	0	3.987
30	KIDNE20091090	0	100
	KIDNE20094260	0	100
	KIDNE20094670	0	59.494
	KIDNE20095530	0	100
	KIDNE20133460	0	100
35	KIDNE20133880	0	100
	KIDNE20134130	0	65.363
	KIDNE20134890	0	100
	KIDNE20137310	0	100
40	KIDNE20138450	0	38.971
	KIDNE20140870	0	22.93
	KIDNE20141120	0	100
	KIDNE20141700	0	100
	KIDNE20142680	0	100
45	KIDNE20142900	0	31.732
	KIDNE20143200	0	100
	KIDNE20147170	0	100
	KIDNE20148080	0	100
	KIDNE20149780	0	60.365
50	KIDNE20150730	0	100
	KIDNE20152440	0	100
	KIDNE20154330	0	100
	KIDNE20154830	0	100
55	KIDNE20155980	0	100
	KIDNE20157100	0	100
	KIDNE20160360	0	100
	KIDNE20160960	0	100

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Table 38 (continued)

	Clone ID	FEKID	KIDNE
5	KIDNE20163710	0	100
	KIDNE20165390	0	100
	KIDNE20169180	0	100
	KIDNE20170400	0	19.556
	KIDNE20173150	0	100
10	KIDNE20173430	0	36.673
	KIDNE20176030	0	100
	KIDNE20181670	0	100
	KIDNE20182540	0	100
	KIDNE20186170	0	100
15	KIDNE20188630	0	100
	KIDNE20189890	0	100
	KIDNE20189960	0	100
	KIDNE20191870	0	100
20	OCBBF20174890	0	32.241
	PLACE60073090	0	10.501
	PLACE60181870	0	49.921
	PROST20016760	0	3.992
	PUAEN10000650	0	6.676
25	SKNMC20006350	24.429	0
	SPLEN20017610	0	42.429
	SPLEN20063250	0	3.996
	SPLEN20126110	0	50.05
30	SPLEN20135030	0	31.695
	TESTI20061200	0	13.537
	TESTI20262150	0	40.96
	THYMU10004280	0	3.534
	THYMU20139160	0	2.704
35	TRACH20011010	0	10.647

Table 39

	Clone ID	FELNG	HLUNG
40	BRAMY20001510	0	5.948
	BRAMY20043630	0	15.102
	BRAMY20204270	0	7.785
	BRAMY20227860	0	1.488
45	CTONG20029030	0	28.504
	CTONG20168460	0	76.291
	CTONG20186290	0	61.67
	FEBRA20039260	0	7.62
50	FEBRA20078800	0	33.686
	FEBRA20163980	0	38.327
	HCHON20000870	0	23.288
	HLUNG20008460	0	67.54
	HLUNG20009260	0	100
55	HLUNG20009550	0	100
	HLUNG20010130	0	100
	HLUNG20011260	0	100

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Table 39 (continued)

Clone ID	FELNG	HLUNG
HLUNG20011440	0	100
HLUNG20011460	0	76.577
HLUNG20012140	0	100
HLUNG20014590	0	36.045
HLUNG20015070	0	17.804
HLUNG20015180	0	4.723
HLUNG20020500	0	100
HLUNG20020850	0	67.488
HLUNG20021450	0	68.006
HLUNG20023030	0	100
HLUNG20024050	0	100
HLUNG20025620	0	100
HLUNG20028110	0	76.618
HLUNG20029420	0	100
HLUNG20029490	0	81.173
HLUNG20030420	0	100
HLUNG20030490	0	100
HLUNG20030610	0	100
HLUNG20031620	0	80.237
HLUNG20032460	0	44.037
HLUNG20033060	0	36.529
HLUNG20033310	0	100
HLUNG20033350	0	100
HLUNG20034970	0	79.349
HLUNG20037140	0	100
HLUNG20037160	0	100
HLUNG20037780	0	44.761
HLUNG20038330	0	100
HLUNG20041540	0	100
HLUNG20041590	0	10.207
HLUNG20042730	0	100
HLUNG20045340	0	7.67
HLUNG20047070	0	100
HLUNG20050760	0	100
HLUNG20051330	0	100
HLUNG20052300	0	23.611
HLUNG20054790	0	100
HLUNG20055240	0	100
HLUNG20056560	0	75.961
HLUNG20057380	0	100
HLUNG20059240	0	100
HLUNG20060670	0	100
HLUNG20063700	0	100
HLUNG20065700	0	62.8
HLUNG20065990	0	100
HLUNG20067810	0	100
HLUNG20068120	0	50.947
HLUNG20069350	0	100
HLUNG20070410	0	100
HLUNG20072100	0	54.241

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Table 39 (continued)

Clone ID	FELNG	HLUNG
HLUNG20072190	0	79.349
HLUNG20072450	0	7.744
HLUNG20074330	0	100
HLUNG20079310	0	100
HLUNG20081390	0	66.429
HLUNG20081530	0	100
HLUNG20082350	0	100
HLUNG20083330	0	100
HLUNG20083480	0	13.123
HLUNG20083840	0	100
HLUNG20083960	0	40.76
HLUNG20084790	0	100
HLUNG20085210	0	50.993
HLUNG20088750	0	100
HLUNG20092530	0	100
HLUNG20093030	0	100
HLUNG20094130	0	75.987
KIDNE20142900	0	68.268
PROST20016760	0	8.589
PROST20052850	0	57.701
SKNMC20006350	0	2.134
SMINT20035050	0	6.135
SPLEN20012450	0	25.695
TESTI20057590	0	17.804
TESTI20061200	0	29.123
TESTI20067480	0	18.856
TESTI20116050	0	30.168
THYMU10004280	0	7.603
THYMU20010180	0	79.349
THYMU20139160	0	1.939
TRACH20011010	0	22.907
UTERU20016580	0	43.64
UTERU20127030	0	66.318

Table 40

<p>Alteration of the expression level of each clone due to TNF-α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with <i>Helicobacter pylori</i>. ctl, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF-α for 1 hour, and in the cell stimulated with 10 ng/mL TNF-α for 3 hours; ctl, Hp, and ΔcagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without <i>Helicobacter pylori</i>, in the cells co-cultured with cag PAI-positive <i>Helicobacter pylori</i> (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2ΔcagE) (at a ratio of MKN45 : TN2ΔcagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]</p>						
Clone name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	Δ cagE
ASTR020045840	1.5	2.3	1.9	2.3	2.4	0.2
ASTR020055930	0.8	1.9	1.4	0.8	0.8	0.5

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Table 40 (continued)

	Clone name	THP-1			MKN45		
		ctl	TNF_1h	TNF_3h	ctl	Hp	Δ cagE
5	ASTR020088950	1.0	0.2	2.5	1.1	0.3	0.3
	BNGH420052350	2.2	2.2	0.0	0.5	0.5	3.2
	BRACE20052530	2.6	1.0	0.3	2.2	1.0	0.9
	BRACE20054080				0.8	1.1	1.0
10	BRAMY20003880	1.5	0.9	0.6	1.2	0.0	1.3
	BRAMY20027390	0.6	4.2	0.1	2.9	0.4	0.1
	BRAMY20028530				0.5	3.4	4.1
	BRAMY20035380	1.3	0.9	0.8	0.5	1.7	0.5
	BRAMY20036530				1.1	0.3	0.3
15	BRAMY20050940	0.4	0.0	0.0	0.2	0.2	1.0
	BRAMY20072440				0.5	0.5	0.1
	BRAMY20096930	3.8	5.2	4.7	1.7	2.4	1.7
	BRAMY20118410	0.8	3.7	0.8	2.7	0.0	0.0
20	BRAMY20237190	0.0	2.3	0.1			
	BRAWH20055330	2.5	4.7	2.8	1.2	1.3	0.0
	BRAWH20078620				1.9	1.2	1.0
	BRAWH20190530	0.6	0.1	0.0	0.3	0.0	0.0
	BRCAN20001480	1.0	3.4	4.1	1.4	1.6	0.6
25	BRHIP10000720	0.3	1.8	1.4	0.9	0.0	1.7
	BRHIP10001040	0.9	0.7	0.1	0.0	0.1	0.0
	BRHIP20000210	0.6	0.6	0.0	2.0	0.3	0.0
	BRSSN20001970	0.8	1.4	1.3	0.8	0.7	0.5
	BRSSN20091190				0.6	0.1	0.8
30	CD34C20001750	0.0	0.4	2.0			
	CTONG20078340	0.3	2.6	1.6	0.9	0.7	2.4
	CTONG20079590	1.0	1.2	0.2	0.1	0.0	0.0
	CTONG20083980	0.0	0.0	0.0	1.3	1.8	1.9
35	CTONG20085210	0.8	1.2	2.3	0.1	0.2	0.1
	DFNES20063460	1.7	3.6	2.7	1.3	2.0	0.1
	DFNES20072990	1.4	1.9	2.0	5.0	4.9	4.2
	FCBBF20029280	1.8	5.5	3.8	2.3	2.2	2.3
40	FCBBF20032930	0.1	0.1	0.0	1.7	0.5	0.5
	FCBBF20036360	0.6	0.7	0.4	0.4	0.2	0.2
	FCBBF30022680	2.9	1.0	0.3	2.9	1.0	0.3
	FCBBF30078600	1.1	2.6	0.6			
	FCBBF30105080	1.8	1.6	1.9	0.2	0.1	0.0
45	FCBBF30169870	1.1	1.2	0.2	1.6	0.3	0.3
	FCBBF30225930	2.2	0.8	1.0	1.1	0.7	0.2
	FCBBF50000610	2.1	2.8	2.2	2.0	2.2	1.3
	FEBRA20007820	0.0	1.7	2.4	2.1	1.4	1.2
	FEBRA20031280	0.1	1.8	4.5	0.5	0.0	0.0
50	FEBRA20031810	1.4	3.9	3.5	1.5	2.1	1.9
	FEBRA20039260	2.0	3.0	2.5			
	FEBRA20046280	1.3	0.3	0.3			
	FEBRA20084750				2.5	2.2	0.3
55	FEBRA20182030	3.0	4.0	4.2	1.6	0.3	0.7
	HLUNG20041540	0.0	2.2	2.2	1.9	2.4	0.2
	HLUNG20092530	0.3	0.3	3.1	0.2	0.2	0.9

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Table 40 (continued)

	Clone name	THP-1			MKN45		
		ctl	TNF_1h	TNF_3h	ctl	Hp	ΔcagE
5	KIDNE20084030	1.6	0.1	0.3	0.1	0.0	0.0
	KIDNE20084800	0.6	0.3	0.0	0.5	0.5	1.1
	KIDNE20134130	0.4	0.4	0.5	2.3	1.2	1.6
	KIDNE20182540				1.1	0.3	0.3
10	KIDNE20186170	0.0	0.0	0.0	0.6	0.0	0.0
	KIDNE20188630	1.5	0.5	0.5	0.4	0.3	0.0
	LIVER20007750	1.3	1.8	0.3	1.9	0.7	0.0
	MESAN20021220	1.7	2.6	1.6	2.3	0.9	0.3
	MESAN20084150	0.8	2.6	2.2	1.7	2.1	1.1
15	NT2NE20059210				1.4	0.4	0.1
	NT2NE20082130	1.8	1.3	0.5	1.9	0.3	0.3
	NT2NE20092950	1.3	2.7	3.4	1.7	2.4	1.8
	NT2RP70031070	0.3	0.9	1.4	0.4	0.4	0.0
20	OCBBF20012520	0.3	0.3	1.3	0.9	0.2	1.2
	OCBBF20110210	4.5	1.8	0.5	0.5	0.5	4.5
	OCBBF20110730	0.4	0.5	0.3	0.1 1	0.0	0.0
	OCBBF20155030	1.1	1.1	0.9	2.5	0.8	0.3
	OCBBF20165900	1.7	4.4	4.4	1.9	3.3	1.1
25	OCBBF20170350	0.9	5.4	0.3	0.3	1.7	1.5
	OCBBF20176650	0.5	1.3	0.5	0.7	0.7	0.0
	PLACE60006300	0.8	3.2	1.0	0.5	0.5	0.9
	PLACE60061370	2.7	0.8	1.5	1.2	1.0	1.3
30	PROST20011160	0.2	1.7	2.0	1.3	5.5	1.7
	PROST20041460	2.9	0.1	1.5	0.6	0.0	0.0
	PROST20065100	1.4	1.9	1.6	5.3	0.0	0.0
	PROST20075280	1.7	0.5	0.5	2.6	0.5	0.5
	PROST20106060	0.2	0.2	2.0	1.0	0.6	0.7
35	PROST20110120	1.2	0.6	0.5			
	SKMUS20091900	1.2	1.6	0.3	1.2	2.6	0.3
	SMINT20024140				0.0	0.1	0.0
	SMINT20092160	0.5	0.7	0.3	1.3	1.2	0.3
40	SPLEN20040780	1.0	2.8	1.9	0.3	0.8	0.1
	SPLEN20110860	2.4	0.1	7.6	1.4	0.1	0.1
	SPLEN20177400	0.8	3.3	1.3	1.3	0.7	0.3
	TESTI20038240				0.1	0.0	0.0
	TESTI20043130	0.0	0.1	0.7			
45	TESTI20046540	1.1	0.8	0.2	1.1	0.8	0.3
	TESTI20047370	0.4	0.4	0.5	0.6	0.0	0.5
	TESTI20057200	2.5	0.0	1.2	1.1	0.4	0.3
	TESTI20057590	0.1	0.1	0.0	3.8	3.5	2.2
	TESTI20113940	5.2	0.2	0.2	4.4	0.4	0.4
50	TESTI20149880				2.2	0.2	2.2
	TESTI20151800	2.1	3.3	2.3	2.5	1.0	0.3
	TESTI20173050	0.8	0.6	0.5	1.8	1.1	1.0
	TESTI20198600				2.2	0.2	2.2
55	TESTI20257910	1.2	0.3	0.3	1.2	0.2	0.7
	TESTI20262940	1.5	1.1	0.2	1.1	1.3	0.2
	THYMU20046770				1.7	0.5	0.5

Table 40 (continued)

Clone name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	Δ cagE
THYMU20058550				1.9	0.1	0.1
THYMU20062520	0.0	0.0	0.7	0.2	0.3	0.1
THYMU20062770				1.6	1.0	0.3
THYMU20078240	0.3	1.7	2.9	0.0	1.0	0.1
THYMU20150190	0.2	0.2	0.6	1.4	0.5	1.9
TRACH20125620	1.1	2.5	1.5	1.4	1.4	1.0
TRACH20149740	9.4	9.4	0.9	1.6	2.1	0.6
TRACH20190460	2.0	3.3	3.1	0.2	1.1	0.2
UTERU20045200	1.4	2.6	3.9	0.9	2.1	2.5
UTERU20064120	0.6	2.7	2.0	0.6	1.7	0.4
UTERU20103200	0.1	0.0	0.9	2.4	1.7	0.9
ADRL20046760				0.5	0.5	0.5
ASTRO20055530	0.7	2.4	1.7	0.8	2.1	1.6
BRAMY20076130	0.1	1.4	0.2	0.1	0.0	0.0
CTONG20170940	1.6	0.8	0.3	0.5	9.9	0.5
FCBBF20033360	0.1	0.4	1.4	6.4	0.3	0.7
FCBBF30257370	2.7	0.3	0.3	2.2	0.1	2.2
FCBBF50001650	1.0	1.6	1.2	1.3	1.0	0.9
FEBRA20040290	0.4	1.9	1.1	0.4	1.5	1.4
FEBRA20063720	2.9	3.3	3.1	1.5	0.7	1.4
FEBRA20098040	2.5	2.1	1.5	4.2	0.0	0.3
FEBRA20108580	1.4	2.8	2.8	0.7	0.2	0.2
MESAN20021860	0.1	1.2	0.2	0.9	1.0	0.9
MESAN20067430	0.8	3.0	1.5	0.0	0.3	0.0
NT2NE20045190	0.7	0.2	0.2	0.8	0.6	0.2
PROST20016760				1.1	3.4	2.3
SKNSH20007160	0.6	0.3	0.2	1.1	0.7	0.6
SMINT20006020	2.5	1.0	0.3	2.4	0.3	0.3
TESTI20059370	0.0	0.2	0.3	0.0	0.0	0.0
TESTI20103690	0.0	0.0	0.0	0.8	0.3	0.3
TESTI20254480	0.0	0.1	0.6	0.8	0.6	0.0
THYMU10004280	0.2	2.2	0.2	0.2	1.1	1.4
THYMU20030460	0.2	0.6	0.2	0.6	0.8	2.4
TRACH20090060	0.5	0.3	2.0	0.0	6.8	1.7
UTERU20041970	1.6	1.1	1.5	0.0	3.5	2.4
BRAMY20125360	0.8	1.6	1.1	0.0	0.0	0.0
OCBBF20142290	0.2	0.9	0.3	0.1	0.4	0.0
SKMUS20006790	0.7	0.5	0.3	1.0	0.8	0.7
TESTI20030610	0.1	2.0	1.7	0.0	0.3	0.0
UTERU20026620	0.4	4.2	4.2	2.4	2.7	0.9

Homology Search Result Data

[0313] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences.

[0314] In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared.

[0315] Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

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- ADRGL20020290//Human placental equilibrative nucleoside transporter 1 (hENT1) mRNA, complete cds.//1.70E-240//456aa//100%//U81375
- ADRGL20021910//Homo sapiens transmembrane protein B7-H2 ICOS ligand mRNA, complete cds.//2.50E-88//168aa//100%//AAG01176
- 5 ADRGL20022600//DIAPHANOUS PROTEIN HOMOLOG 1 (P140MDIA).//2.00E-07//121aa//36%//008808
- ADRGL20023920//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.40E-98//467aa//45%//Q92338
- ADRGL20026790//Homo sapiens PLIC-1 mRNA, complete cds.//6.10E-05//169aa//31%//AF293384
- ADRGL20027530
- ADRGL20036380
- 10 ADRGL20036840//HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR (HLA-AR) (HLA-12.4).//7.30E-68//131aa//96%//P01893
- ADRGL20040310
- ADRGL20040770
- ADRGL20046760
- 15 ADRGL20047080
- ADRGL20047770
- ADRGL20057560
- ADRGL20059610//GLUCOSYLCERAMIDASE PRECURSOR (EC 3.2.1.45) (BETA-GLUCOCEREBROSIDASE) (ACID BETA-GLUCOSIDASE) (D-GLUCOSYL-N-ACYLSPHINGOSINE GLUCOHYDROLASE) (ALGLUCERASE) (IMIGLUCERASE).//3.00E-94//188aa//93%//P04062
- 20 ADRGL20062330//Homo sapiens trabeculin-alpha mRNA, complete cds.//1.10E-128//439aa//58%//AF141968
- ADRGL20063770
- ADRGL20066770//elastin microfibril interface located protein [Homo sapiens].//3.00E-31//210aa//44%//NP_008977
- ADRGL20067320
- 25 ADRGL20079060//Mus musculus mRNA for Ky protein (muscle-specific protein).//3.80E-266//281aa//84%//AJ293727
- ADRGL20095330
- ASTRO20001910//Rattus norvegicus mRNA for annexin V-binding protein (ABP-10), partial cds.//2.20E-57//153aa//73%//D64062
- ASTRO20003720
- 30 ASTRO20004820
- ASTRO20006530//Homo sapiens hook1 protein (HOOK1) mRNA, complete cds.//1.80E-94//383aa//55%//AF044923
- ASTRO20009140//PUTATIVE COMPETENCE-DAMAGE PROTEIN.//2.70E-06//167aa//29%//P46323
- ASTRO20010010
- ASTRO20010290
- 35 ASTRO20012270
- ASTRO20020240
- ASTRO20020350
- ASTRO20022020
- ASTRO20026320//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.80E-47//432aa//33%//P30771
- 40 ASTRO20027330
- ASTRO20038400//Homo sapiens zinc finger homeobox protein ZHX1 mRNA, complete cds.//3.40E-78//282aa//42%//AF106862
- ASTRO20045840
- 45 ASTRO20046280//PSU1 PROTEIN.//1.30E-42//228aa//36%//P53550
- ASTRO20047510
- ASTRO20050810//L-RIBULOKINASE (EC 2.7.1.16).//1.10E-43//512aa//30%//P94524
- ASTRO20052420//PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE).//4.80E-151//408aa//76%//Q12774
- 50 ASTRO20053430//BAND 4.1-LIKE PROTEIN 4 (NBL4 PROTEIN).//1.80E-58//307aa//38%//057457
- ASTRO20055530
- ASTRO20055570//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C) (ASCR).//5.40E-72//137aa//100%//P04156
- ASTRO20055930
- 55 ASTRO20058960//DNA damage inducible protein homolog - fission yeast (Schizosaccharomyces pombe)//1.90E-14//205aa//31%//T39541
- ASTRO20069200
- ASTRO20075150//TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)

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(CRAF1) (CD40 BINDING PROTEIN) (CD40BP) (LMP1 ASSOCIATED PROTEIN) (LAP1).//1.00E-25//60aa//98%//Q13114
 ASTRO20076660
 ASTRO20085080//TIPD PROTEIN.//1.80E-58//307aa//37%//015736
 5 ASTRO20088950//LACTASE-PHLORIZIN HYDROLASE PRECURSOR (LACTASE-GLYCOSYLCERAMIDASE) [INCLUDES: LACTASE (EC 3.2.1.108); PHLORIZIN HYDROLASE (EC 3.2.1.62)].//7.80E-85//331aa//48%//P09848
 ASTRO20089600//Mus musculus saccin gene, complete cds.//1.10E-05//198aa//26%//AF193557
 ASTRO20090680//M.musculus mRNA for IB3/5-polypeptide.//1.60E-173//412aa//78%//X79131
 ASTRO20091180
 10 ASTRO20091770
 ASTRO20141740
 BGGI120000670//Rattus norvegicus myosin heavy chain Myr 8b mRNA, complete cds.//1.660E-05//86aa//36%//AY004215
 BGGI120010750//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene).//7.90E-305//812aa//71%//AJ251245
 15 BNGH410000570
 BNGH420008150//Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds.//3.40E-139//326aa//82%//U07747
 BNGH420014060
 20 BNGH420015760//Mus musculus mRNA for JNK-binding protein JNKBP1, complete cds.//1.60E-130//381aa//60%//AB029482
 BNGH420021680
 BNGH420023870//RIBONUCLEASE INHIBITOR.//4.70E-41//314aa//34%//P10775
 BNGH420024870
 25 BNGH420035290//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//7.60E-37//273aa//35%//P90648
 BNGH420036410
 BNGH420040760
 BNGH420042910
 BNGH420045380
 30 BNGH420046790//immunoglobulin lambda light chain variable region [Homo Sapiens].//5.00E-47//84aa//100%//AAG24674
 BNGH420052350
 BNGH420059680//DIPZ PROTEIN.//3.00E-13//166aa//31%//Q10801
 BNGH420061350
 35 BNGH420062340
 BNGH420070370//ZINC FINGER PROTEIN GLI1 (GLI).//3.20E-65//165aa//59%//P47806
 BNGH420074600//DNA-DIRECTED RNA POLYMERASE III 128 KDA POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//5.40E-214//522aa//72%//P25167
 BNGH420075940
 40 BNGH420077980//Rattus norvegicus ankyrin binding cell adhesion molecule neurofascin mRNA, alternatively spliced form, partial cds.//0//588aa//98%//U81036
 BNGH420085100
 BNGH420086030//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//2.30E-21//130aa//40%//P15882
 45 BNGH420087430//Mus musculus mRNA 1 for phtf protein.//5.80E-118//237aa//57%//AJ133721
 BRACE10000510//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//4.70E-12//132aa//37%//P26371
 BRACE20003310//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.00E-205//504aa//71%//Q03923
 50 BRACE20007330//RING CANAL PROTEIN (KELCH PROTEIN).//4.60E-66//562aa//31%//Q04652
 BRACE20009050
 BRACE20014450//Mus musculus mRNA for Ndr1 related protein Ndr2, complete cds.//3.20E-150//291aa//95%//AB033921
 BRACE20017790
 55 BRACE20018810
 BRACE20025820
 BRACE20038920
 BRACE20050870//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//8.40E-59//584aa//31%//P32639

- BRACE20051600
 BRACE20051930//NEUROPILIN PRECURSOR (A5 PROTEIN) (A5 ANTIGEN).//5.50E-20//179aa//30%/P28824
 BRACE20052430//Homo sapiens AMSH mRNA, complete cds.//4.30E-75//272aa//53%/U73522
 BRACE20052530
 5 BRACE20054080
 BRACE20054480
 BRACE20054600//Xenopus laevis mRNA for Kielin, complete cds.//4.30E-70//205aa//60%/AB026192
 BRACE20055560
 BRACE20057870
 10 BRACE20059110
 BRACE20059810
 BRACE20061620//ZINC-BINDING PROTEIN A33.//3.60E-30//329aa//28%/Q02084
 BRACE20062580
 BRACE20063540//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//1.60E-10//164aa//35%/P09125
 15 BRACE20065470//Xenopus laevis ubiquitin-like fusion protein mRNA, complete cds.//6.70E-63//170aa//71%/L08474
 BRACE20066360
 BRACE20068710
 BRACE20069000//CLN3 PROTEIN (BATTENIN) (BATTEN'S DISEASE PROTEIN).//1.20E-147//279aa//100%/Q13286
 20 BRACE20069110
 BRACE20069440
 BRACE20079200//Xenopus laevis mRNA for Kielin, complete cds.//3.10E-15//63aa//58%/AB026192
 BRACE20079370//microtubule associated-protein orbit [Drosophila melanogaster].//8.00E-42//282aa//36%/BAA94248
 25 BRACE20097540//Homo sapiens protein serine/threonine phosphatase 4 regulatory subunit 1 (PP4R1) mRNA, complete cds.//2.80E-96//193aa//96%/AF111106
 BRACE20098860
 BRACE20099070
 BRACE20194670//UDP-GALACTOSE TRANSLOCATOR (UDP-GALACTOSE TRANSPORTER) (UGT) (UDP-GAL-TR).//1.40E-32//72aa//98%/P78381
 30 BRACE20196180//Homo sapiens HMG domain protein HMGX2 (HMGX2) mRNA, complete cds.//6.90E-154//235aa//91%/AF146223
 BRACE20196960
 BRACE20200770//PROTEIN MOV-10.//3.30E-24//113aa//50%/P23249
 35 BRACE20200970
 BRACE20204670//PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURSOR (EC 3.1.3.48) (R-PTP- ALPHA).//4.30E-237//428aa//99%/P18433
 BRACE20205840
 BRACE20207420
 40 BRACE20212450
 BRACE20215410//PROTEIN-TYROSINE PHOSPHATASE YVH1 (EC 3.1.3.48) (PTPASE YVH1).//2.90E-08//136aa//31%/Q02256
 BRACE20216700
 BRACE20216950//4F2 CELL-SURFACE ANTIGEN HEAVY CHAIN (4F2HC) (LYMPHOCYTE ACTIVATION ANTIGEN 4F2 LARGE SUBUNIT) (4F2 HEAVY CHAIN ANTIGEN) (CD98 ANTIGEN).//4.80E-66//94aa//90%/P08195
 45 BRACE20219360
 BRAMY10000980
 BRAMY10001730
 BRAMY20000210
 50 BRAMY20000250
 BRAMY20001510//Homo sapiens RING zinc finger protein (RZF) mRNA, complete cds.//3.80E-131//245aa//99%/AF037204
 BRAMY20003540//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//0//745aa//99%/P51178
 55 BRAMY20003880
 BRAMY20005080//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M).//2.70E-46//93aa//100%/Q9Y5T5

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BRAMY20013670//PECANEX PROTEIN.//1.80E-84//300aa//56%//P18490
 BRAMY20016780
 BRAMY20020440
 BRAMY20021580
 5 BRAMY20023390
 BRAMY20023640
 BRAMY20024790
 BRAMY20027390
 BRAMY20027990//Homo sapiens NEDL1 mRNA for NEDD4-like ubiquitin ligase 1, complete cds.//4.60E-158//294aa//
 10 100%//AB048365
 BRAMY20028530
 BRAMY20028620//NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE [CARBOXYLATING] (EC 2.4.2.19) (QUINOLINATE PHOSPHORIBOSYLTRANSFERASE [DECARBOXYLATING]) (QAPRTASE).//9.70E-18//53aa//84%//Q15274
 15 BRAMY20035380//ZINC TRANSPORTER 1 (ZNT-1).//5.60E-40//211aa//35%//Q62720
 BRAMY20035830//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//3.60E-103//251aa//75%//AF060219
 BRAMY20036530
 BRAMY20036810
 20 BRAMY20038980//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//3.40E-17//407aa//23%//P25386
 BRAMY20039290
 BRAMY20040580//ZINC FINGER PROTEIN 135.//1.70E-29//115aa//54%//P52742
 BRAMY20043520
 BRAMY20043630//Homo sapiens Ras-binding protein SUR-8 mRNA, complete cds.//1.30E-167//364aa//88%//AF068920
 25 BRAMY20044920//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG.//7.60E-28//86aa//4796//Q13107
 BRAMY20045210
 30 BRAMY20045420
 BRAMY20047560
 BRAMY20050640
 BRAMY20050940
 BRAMY20051820//Human mRNA for Doc2 (Double C2), complete cds.//1.90E-49//102aa//99%//D31897
 35 BRAMY20052440
 BRAMY20053910
 BRAMY20055760//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE VA (EC 3.6.1.-).//5.80E-130//393aa//59%//054827
 BRAMY20056620//Homo sapiens mccb mRNA for non-biotin containing subunit of 3-methylcrotonyl-CoA carboxylase, complete cds.//3.00E-106//203aa//100%//AB050049
 40 BRAMY20056840//UBE-1c2//2.40E-74//261aa//53%//AB030505
 BRAMY20063750//Homo sapiens HRIHFB2007 mRNA, partial cds.//3.40E-139//253aa//99%//AB015330
 BRAMY20072440
 BRAMY20072870//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE—COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.50E-15//88aa//46%//P16929
 45 BRAMY20073080
 BRAMY20074110
 BRAMY20074860
 BRAMY20076100//STEROIDOGENIC FACTOR 1 (STF-1) (SF-1) (STEROID HORMONE RECEPTOR AD4BP) (FUSHI TARAZU FACTOR HOMOLOG 1).//4.80E-66//132aa//94%//P50569
 50 BRAMY20076130
 BRAMY20076530
 BRAMY20083330//SYNAPSIN I.//4.50E-05//155aa//29%//P17599
 BRAMY20083820
 55 BRAMY20089770//P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RECEPTOR).//3.30E-136//242aa//99%//Q99572
 BRAMY20091230//MITOCHONDRIAL UNCOUPLING PROTEIN 4 (UCP 4).//4.60E-121//224aa//100%//095847
 BRAMY20093490//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//7.80E-43//139aa//

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- 55%//AF061555
BRAMY20094890//A KINASE ANCHOR PROTEIN 4 PRECURSOR (MAJOR FIBROUS SHEATH PROTEIN) (FSC1) (P82).//4.60E-06//131aa//27%//Q60662
BRAMY20095080
- 5 BRAMY20095570
BRAMY20096930//Torpedo marmorata mRNA for male sterility protein 2-like protein (ms21 gene).//2.00E-63//139aa//82%//AJ272073
BRAMY20100680
BRAMY20102900//Homo sapiens RU1 (RU1) mRNA, complete cds.//1.20E-47//151aa//58%//AF168132
- 10 BRAMY20107980
BRAMY20111780//ZINC FINGER PROTEIN 135.//1.00E-139//416aa//57%//P52742
BRAMY20117670//Mus musculus mmDNAJA4 mRNA for mmDj4, complete cds.//3.20E-118//239aa//90%//AB032401
BRAMY20118410
BRAMY20118490//GLYCEROL KINASE 2 (EC 2.7.1.30) (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE 2) (GLYC-EROKINASE 2) (GK 2).//1.80E-48//247aa//40%//Q9X1E4
- 15 BRAMY20120170
BRAMY20123400
BRAMY20124970
BRAMY20125170
- 20 BRAMY20125360//L-ASPARAGINASE (EC 3.5.1.1) (L-ASPARAGINE AMIDOHYDROLASE).//3.30E-53//148aa//43%//Q9ZSD6
BRAMY20125550//Homo sapiens mRNA for 28kD interferon responsive protein (IFRG28 gene).//4.40E-16//155aa//33%//AJ251832
BRAMY20126910
- 25 BRAMY20127310
BRAMY20127760
BRAMY20134050//NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 2 (BRAIN-SPECIFIC PROTEIN, X- LINKED).//1.40E-25//109aa//569d//P51860
BRAMY20135720
- 30 BRAMY20137360//Homo sapiens gene for TU12B1-TY, exon 12 and complete cds.//2.10E-18//257aa//31%//AB032786
BRAMY20139440
BRAMY20139750
BRAMY20143870//PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) (PTH).//5.80E-27//182aa//35%//P96386
- 35 BRAMY20152510//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEU-RAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT).//4.80E-293//537aa//97%//P54829
BRAMY20155500
BRAMY20158550//CALMODULIN.//1.60E-15//116aa//42%//P04352
BRAMY20159250
- 40 BRAMY20160020
BRAMY20173480
BRAMY20190550//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//2.20E-226//464aa//89%//P42566
BRAMY20194680
- 45 BRAMY20204270
BRAMY20206340//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//4.20E-07//151aa//27%//P38011
BRAMY20219620
BRAMY20221600//H.sapiens mRNA for novel T-cel activation protein.//1.60E-130//245aa//99%//X94232
- 50 BRAMY20223010//Mus musculus leucine-rich glioma-inactivated 1 protein precursor, (Lgi1) mRNA, complete cds.//2.00E-79//269aa//52%//AF246818
BRAMY20225250
BRAMY20225320
BRAMY20227230
- 55 BRAMY20227860//Homo sapiens dickkopf-3 (DKK-3) mRNA, complete cds.//2.30E-69//147aa//92%//AF177396
BRAMY20227960
BRAMY20231150//PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).//2.30E-55//322aa//39%//Q09549
BRAMY20234820//Homo sapiens mitotic checkpoint protein (MAD1) mRNA, complete cds.//1.30E-286//561aa//

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100%//AF123318
 BRAMY20237190
 BRAMY20238630//TETRATRICOPEPTIDE REPEAT PROTEIN 4.//1.20E-147//276aa//99%//095801
 BRAMY20243120
 5 BRAMY20244490//ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE).//2.50E-19//119aa//37%//P00571
 BRAMY20245140//Rattus norvegicus potassium channel (erg2) mRNA, complete cds.//1.00E-178//427aa//81%//AF016192
 BRAMY20245350
 10 BRAMY20245760//Araneus diadematus fibroin-4 mRNA, partial cds.//7.90E-05//285aa//22%//U47856
 BRAMY20251210//EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3) (EMBRYONIC BRAIN KINASE) (EBK) (DEVELOPMENTAL KINASE 1) (MDK-1).//3.80E-94//268aa//66%//Q61772
 BRAMY20251750//Homo sapiens BRI3 mRNA, complete cds.//2.80E-131//242aa//95%//AF272043
 15 BRAMY20263000//DYSTROPHIA MYOTONICA-CONTAINING WD REPEAT MOTIF PROTEIN (DMR-N9 PROTEIN).//2.60E-134//430aa//59%//Q08274
 BRAMY20267780
 BRAMY20269040
 BRAMY20271140
 20 BRAMY20274510//60S RIBOSOMAL PROTEIN L12.//1.10E-39//102aa//82%//P30050
 BRAMY2028565Q
 BRAMY20287400
 BRAWH20014590//ZAKI-4 PROTEIN.//3.10E-92//187aa//93%//Q14206
 BRAWH20020470
 25 BRAWH20020600
 BRAWH20021910//FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE B).//1.30E-111//450aa//49%//Q04791
 BRAWH20025490
 BRAWH20026010//AD021 protein [Homo sapiens]//4.00E-55//245aa//44%//NP_057697
 30 BRAWH20027250
 BRAWH20030000
 BRAWH20039640//SLIT PROTEIN PRECURSOR.//6.10E-19//282aa//31%//P24014
 BRAWH20040680//PUTATIVE TRANSCRIPTION ELONGATION FACTOR S-II (TFIIS).//5.90E-06//179aa//29%//P52652
 35 BRAWH20047790
 BRAWH20050740//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//1.60E-16//235aa//30%//Q60821
 BRAWH20055240
 BRAWH20055330
 40 BRAWH20055780
 BRAWH20058120
 BRAWH20063010//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//2.60E-06//121aa//33%//Q15427
 BRAWH20078080
 45 BRAWH20078620
 BRAWH20080580//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.00E-116//316aa//63%//P51523
 BRAWH20082550
 BRAWH20082920//Human TFIIIC Box B-binding subunit mRNA, complete cds.//1.90E-36//72aa//100%//U02619
 BRAWH20093040//PROTEIN KINASE CLK2 (EC 2.7.1.-).//2.70E-86//162aa//96%//P49760
 50 BRAWH20093070//SYNAPSIN.//4.80E-06//245aa//28%//Q24546
 BRAWH20094900//Mus musculus mRNA for sialidase, complete cds.//5.70E-73//310aa//50%//AB026842
 BRAWH20095900//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.20E-170//631aa//48%//Q99676
 BRAWH20173790
 BRAWH20174330//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//4.50E-06//121aa//33%//Q15427
 55 BRAWH20175230
 BRAWH20175340
 BRAWH20176850//Mus musculus mRNA for nuclear protein ZAP, complete cds.//9.50E-151//619aa//53%//AB033168

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BRAWH20182670
 BRAWH20183170//GRR1 PROTEIN.//9.30E-13//218aa//28%/P24814
 BRAWH20185260
 BRAWH20185270
 5 BRAWH20186010
 BRAWH20188750//BIOTIN SYNTHESIS PROTEIN BIOC.//5.80E-11//190aa//27%/P36571
 BRAWH20190530//Homo sapiens BNPI mRNA for brain-specific Na-dependent inorganic phosphate cotransporter, complete cds.//2.10E-109//118aa//100%/AB032436
 BRAWH20190550//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.30E-05//172aa//29%/P49695
 10 BRAWH20191980//PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR (EC 1.5.3.-) (PROLINE DEHYDROGENASE).//2.10E-125//234aa//99%/O43272
 BRCAN10000760//UREA TRANSPORTER, ERYTHROCYTE.//1.30E-212//389aa//100%/Q13336
 BRCAN10001050//PEANUT-LIKE PROTEIN 2 (BRAIN PROTEIN H5).//1.40E-62//122aa//98%/O43236
 15 BRCAN10001680
 BRCAN20001480
 BRCAN20004180//alpha-1C-adrenergic receptor splice form 2 - human//1.10E-22//76aa//76%/S65657
 BRCAN20005230//HEPARIN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N-DEACETYLASE/N-SULFOTRANSFERASE).//8.90E-15//168aa//28%/P52849
 20 BRCAN20005410//Human 1(3)mbt protein homolog mRNA, complete cds.//2.00E-95//378aa//50%/U89358
 BRCOC10000400
 BRCOC20000470//Homo sapiens DEME-6 mRNA, partial cds.//7.30E-37//252aa//28%/AF007170
 BRCOC20003600//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//5.90E-192//418aa//85%/P40682
 25 BRHIP10000720
 BRHIP10001040//tweety homolog 1 (Drosophila) [Mus musculus]/1.30E-68//311aa//44%/NP_067299
 BRHIP20000210
 BRHIP20003590
 30 BRHIP20005060
 BRSSN20001970
 BRSSN20005610//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.//6.30E-225//730aa//60%/AF127084
 BRSSN20005660
 35 BRSSN20066440//ZINC FINGER PROTEIN 202.//3.60E-37//169aa//37%/O95125
 BRSSN20074640//HYPOTHETICAL 35.8 KDA PROTEIN IN PRP16-SRP40 INTERGENIC REGION.//4.50E-20//217aa//28%/P36163
 BRSSN20091190
 BRSSN20092440
 40 BRSSN20093890//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//8.40E-13//203aa//30%/AB026190
 CD34C20001750//MHC CLASS I NK CELL RECEPTOR PRECURSOR (NATURAL KILLER ASSOCIATED TRANSCRIPT 4) (NEAT-4).//1.10E-18//214aa//3596//P43630
 CTONG10000090
 45 CTONG20000340
 CTONG20002790
 CTONG20004110//Mus musculus ankycorbin mRNA, complete cds.//6.20E-55//1006aa//24%/AF202315
 CTONG20004520//development- and differentiation-enhancing factor 2; PYK2 C terminus-associated protein [Homo Sapiens].//2.00E-86//310aa//81%/NP_003878
 50 CTONG20007660//Rattus norvegicus caspase recruitment domain protein 9 mRNA, complete cds.//7.30E-28//319aa//32%/AF311288
 CTONG20008190//YPT1-RELATED PROTEIN 2.//3.00E-30//160aa//40%/P17609
 CTONG20008460
 CTONG20015240
 55 CTONG20017490//SEMAPHORIN 4A PRECURSOR (SEMAPHORIN B) (SEMA B).//3.10E-273//607aa//82%/Q62178
 CTONG20020660
 CTONG20020950//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN).//

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7.40E-23//258aa//25%//P17141
CTONG20027660
CTONG20029030//Homo sapiens Ras-binding protein SUR-8 mRNA, complete cds.//8.30E-25//402aa//28%//AF068920
5 CTONG20030280//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-12//303aa//25%//Q00808
CTONG20031150
CTONG20031890
CTONG20032930//microtubule associated-protein orbit [Drosophila melanogaster]//1.00E-79//913aa//30%//BAA94248
10 CTONG20033500
CTONG20033610//Rattus norvegicus SNIP-a mRNA, complete cds.//2.50E-145//567aa//41%//AF156981
CTONG20033750//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//1.40E-174//492aa//66%//AF227209
CTONG20035240
15 CTONG20036800
CTONG20036990//BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).//1.10E-10//247aa//27%//Q05793
CTONG20039370
20 CTONG20041150//Streptomyces ansochromogenes strain 7100 SanE (sanE) gene, complete cds.//5.20E-05//133aa//35%//AF228524
CTONG20041260//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.30E-238//602aa//74%//AF062476
CTONG20042640//NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK (DESMOYOKIN) (FRAGMENTS).//0//797aa//7396//Q09666
25 CTONG20044230//Mus musculus zinc finger protein (Mtsh1) mRNA, partial cds.//1.40E-289//601aa//89%//AF191309
CTONG20044870
CTONG20045500//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//2.00E-19//276aa//30%//P48751
CTONG20046690
30 CTONG20049480
CTONG20050490
CTONG20051100//PUTATIVE METHYLTRANSFERASE (EC 2. 1. 1. -).//3.50E-29//72aa//87%//043709
CTONG20051450//testis development protein PRTD [Homo sapiens].//9.00E-50//140aa//85%//AAG33852
CTONG20052780//Homo sapiens mRNA for SH3 binding protein, complete cds.//B.00E-21//125aa//42%//AB005047
35 CTONG20053990//ZINC FINGER PROTEIN 195.//4.30E-08//40aa//75%//014628
CTONG20055670
CTONG20055850//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.10E-99//248aa//78%//AF015264
CTONG20056150
40 CTONG20057750
CTONG20057950
CTONG20059130//Mus musculus prominin-like protein mRNA, partial cds.//7.50E-103//259aa//7796//AF128113
CTONG20060040
CTONG20061290
45 CTONG20062730
CTONG20063770//M-PHASE PHOSPHOPROTEIN 9 (FRAGMENT).//1.80E-96//184aa//100%//Q99550
CTONG20063930//BETA-CHIMAERIN (BETA-CHIMERIN).//3.50E-31//189aa//34%//Q03070
CTONG20065240
CTONG20065680
50 CTONG20066110//Homo sapiens DEME-6 mRNA, partial cds.//8.70E-164//557aa//53%//AF007170
CTONG20068360//MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN (CARNITINE/ACYLCARNITINE TRANSLOCASE) (CAC).//8.00E-30//248aa//35%//P97521
CTONG20069320
CTONG20069420
55 CTONG20070090
CTONG20070720//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//9.20E-25//180aa//33%//P30337
CTONG20070780//SPERM-SPECIFIC ANTIGEN 2 (CLEAVAGE SIGNAL-1 PROTEIN) (CS-1).//1.90E-122//249aa//

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97%/P28290
CTONG20470910//Homo sapiens mRNA for 26S proteasome subunit p55, complete cds.//7.70E-227//400aa//100%//
AB003103
CTONG20071040//BETA CRYSTALLIN B2 (BP).//6.80E-25//195aa//34%/P26775
5 CTONG20071680//HYPOTHETICAL 33.6 KDA PROTEIN IN TDK-PRFA INTERGENIC REGION.//7.40E-14//328aa//
23%/P45869
CTONG20072930//ZINC FINGER PROTEIN 41 (FRAGMENT).//4.10E-216//542aa//69%/P51814
CTONG20073990
CTONG20074000//Mus musculus teashirt 2 (Tsh2) gene, partial cds.//0//1024aa//89%/AF207880
10 CTONG20074170
CTONG20074740
CTONG20076230
CTONG20076810//site-1 protease of sterol regulatory element binding proteins [Cricetulus griseus]//2.80E-245//
463aa//93%/AF078105
15 CTONG20077760//SYNAPSIN I.//1.70E-08//209aa//32%/P17599
CTONG20078340//SUPPRESSOR PROTEIN SRP40.//4.10E-08//282aa//26%/P32583
CTONG20079590//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-)
(ST6GALNACIII) (STY).//1.80E-151//305aa//85%/Q64686
CTONG20080140//HYPOTHETICAL 60.3 KDA PROTEIN R13G10.2 IN CHROMOSOME III.//8.40E-29//179aa//40%//
20 Q21988
CTONG20081840
CTONG20083430
CTONG20083980//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//4.50E-10//113aa//34%/P50552
CTONG20084020
25 CTONG20084660//ZINC FINGER PROTEIN 165.//3.30E-33//142aa//57%/P49910
CTONG20085210//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//3.60E-06//94aa//
34%/P25234
CTONG20133720
CTONG20165590
30 CTONG20165750//SON PROTEIN (SON3).//4.40E-239//427aa//99%/P18583
CTONG20166580
CTONG20167750
CTONG20168240
CTONG20168460
35 CTONG20169040//KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15) (CK 15).//6.00E-112//223aa//
99%/P19012
CTONG20169530
CTONG20170940//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//4.60E-10//
93aa//36%/P80144
40 CTONG20174290//TRICHOHYALIN.//1.30E-07//340aa//21%/P37709
CTONG20174440
CTONG20174580//Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein complete cds.//1.00E-115//
335aa//61%/NP_008994
CTONG20176040//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 (ARD3).//1.70E-34//155aa//43%/P37996
45 CTONG20179390
CTONG20179890
CTONG20179980
CTONG20180620
CTONG20180690
50 CTONG20181350
CTONG20183430//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//4.60E-30//311aa//
32%/Q01484
CTONG20183830//IRLB [Homo sapiens]//1.50E-104//191aa//100%/CAA45013
CTONG20184130
55 CTONG20184830//ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 (ATP-BINDING CASSETTE TRANS-
PORTER 1) (ATP-BINDING CASSETTE 1).//1.30E-63//271aa//47%/P41233
CTONG20186140
CTONG20186290//ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (ALDH CLASS

- 3) //1.50E-74//144aa//100%//P30838
 CTONG20186370//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) //2.60E-52//324aa//33%//P51523
 CTONG20186520//ZINC FINGER PROTEIN MFG-3 //1.40E-197//643aa//53%//P16374
 CTONG20186550//cca3 protein - rat //2.10E-37//141aa//56%//T31081
- 5 CTONG20188080
 CTONG20189000//PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) //1.10E-48//222aa//50%//Q12774
 CTONG20190290//39.1 KDA PROTEIN IN SURE-CYSC INTERGENIC REGION //6.00E-15//132aa//31%//Q57261
 CTONG20190630
- 10 DFNES20016470//Homo sapiens SDP1 protein mRNA, complete cds //4.90E-33//95aa//37%//AF076957
 DFNES20018000//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) //8.70E-23//306aa//30%//P33450
 DFNES20025500//Homo sapiens mRNA for paraplegin-like protein //3.00E-29//68aa//94%//Y18314
 DFNES20028170//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds //1.40E-165//393aa//78%//D14336
- 15 DFNES20029660
 DFNES20032550
 DFNES20043710
 DFNES20046840//FORKHEAD BOX PROTEIN E1 (FORKHEAD-RELATED PROTEIN FKHL15) (THYROID TRANSCRIPTION FACTOR 2) (TTF-2) //6.20E-05//151aa//32%//000358
- 20 DFNES20055400//Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA, complete cds //5.40E-203//413aa//91%//AF053003
 DFNES20057660//GRAVE'S DISEASE CARRIER PROTEIN (GDC) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG) //7.00E-31//247aa//33%//Q01888
- 25 DFNES20063460//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE) //1.90E-23//115aa//43%//P36102
 DFNES20072990//HYPOTHETICAL 46.7 KDA PROTEIN IN HOR7-COX7 INTERGENIC REGION //1.80E-22//310aa//25%//Q04835
 DFNES20073320//Mus musculus RING-finger protein MURF mRNA, complete cds //6.70E-118//362aa//61%//AF294790
- 30 DFNES20076340
 DFNES20080880//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP-ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1) //2.00E-104//486aa//43%//Q10472
- 35 DFNES20088810
 DFNES20094820//coronin-like protein [Schizosaccharomyces pombe] //3.60E-20//333aa//24%//CAB11184
 FCBBF10000230//H. sapiens mRNA from TYL gene //3.30E-155//650aa//51%//X99688
 FCBBF10002200
 FCBBF10004760//Homo sapiens GAP-like protein (N61) mRNA, complete cds //9.10E-82//412aa//44%//AF251038
- 40 FCBBF20018680//RABPHILIN-3A //1.70E-16//262aa//30%//P47709
 FCBBF20020440
 FCBBF20021110
 FCBBF20023490//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C //1.20E-90//505aa//39%//042643
- 45 FCBBF20028980
 FCBBF20029280
 FCBBF20032930
 FCBBF20033360//RING CANAL PROTEIN (KELCH PROTEIN) //7.40E-33//234aa//32%//Q04652
 FCBBF20035430//Mus musculus arsenite inducible RNA associated protein (Airap) mRNA, complete cds //1.50E-51//152aa//57%//AF224494
- 50 FCBBF20035490//GAP-associated tyrosine phosphoprotein p62 (Sam68) [Homo sapiens] >pirIIA38219 GAP-associated tyrosine phosphoprotein p62 //1.50E-214//415aa//93%//NP_006550
 FCBBF20036360
 FCBBF20038230
- 55 FCBBF20038950
 FCBBF20041380
 FCBBF20043730
 FCBBF20054390

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FCBBF20056580//Mus musculus NSD1 protein mRNA, complete cds.//3.40E-304//773aa//75%//AF064553
 FCBBF20059660
 FCBBF20061310
 FCBBF20066340//Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds.//1.20E-68//312aa//
 5 49%//U93181
 FCBBF20070800
 FCBBF20070950//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE
 PROTEINS ALPHA, BETA, DELTA AND GAMMA].//5.00E-10//601aa//20%//P40631
 FCBBF30000010
 10 FCBBF30001020
 FCBBF30001100//CRAG protein [Drosophila melanogaster].//7.40E-185//800aa//46%//CAA76938
 FCBBF30001150
 FCBBF30002270//HISTONE H1' (H1.0) (H1(0)).//4.90E-62//154aa//84%//P07305
 FCBBF30002280//THIOREDOXIN PEROXIDASE 2 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 2)
 15 (PROLIFERATION-ASSOCIATED PROTEIN PAG) (NATURAL KILLER CELL ENHANCING FACTOR A) (NKEF-A).//
 1.20E-27//61aa//98%//Q06830
 FCBBF30002330
 FCBBF30003810//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.10E-93//313aa//53%//
 Q05481
 20 FCBBF30004340//Homo sapiens GalNAc-T9 mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase,
 complete cds.//1.60E-109//299aa//63%//AB040672
 FCBBF30004730
 FCBBF30005180
 FCBBF30005360//Mus musculus spermatogenesis associated factor (SPAF) mRNA, complete cds.//0//894aa//84%//
 25 AF049099
 FCBBF30005500//HYPOTHETICAL PROTEIN KIAA0167.//5.80E-16//124aa//36%//Q99490
 FCBBF30019140//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 3 (CHD-3) (MI-2 AUTOANTIGEN 240
 KDA PROTEIN) (MI2-ALPHA).//0//725aa//82%//Q12873
 FCBBF30019180//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A, AL-
 30 PHA ISOFORM (PP2A, SUBUNIT A, PR65-ALPHA ISOFORM) (PP2A, SUBUNIT A, R1-ALPHA ISOFORM).//4.60E-
 233//451aa//98%//P54612
 FCBBF30019240
 FCBBF30021900//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//4.10E-161//633aa//48%//
 Q05481
 35 FCBBF30022680//putative 5'-3' exonuclease//9.00E-12//200aa//25%//AAG29662
 FCBBF30026580//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.//7.60E-27//
 367aa//28%//AF180425
 FCBBF30029250//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.00E-18//754aa//23%//P08640
 40 FCBBF30035570
 FCBBF30042610//Homo sapiens CTL2 gene.//2.10E-137//393aa//60%//AJ245621
 FCBBF30048420//TBX19 PROTEIN (T-BOX PROTEIN 19).//1.40E-94//212aa//85%//060806
 FCBSF30053300//Human autoantigen pericentriol material 1 (PCM-1) mRNA, complete cds.//0//708aa//90%//L27841
 FCBBF30056980
 45 FCBBF30062490//Mus musculus prominin-like protein mRNA, partial cds.//7.70E-85//210aa//79%//AF128113
 FCBBF30063990
 FCBBF30068210
 FCBBF30071500//Homo sapiens dentin phosphoryn mRNA, complete cds.//2.80E-09//675aa//22%//AF094508
 FCBBF30072440//Homo sapiens SARDH mRNA, alternatively spliced, complete cds.//1.70E-14//81aa//53%//
 50 AF095737
 FCBBF30072480
 FCBBF30074530
 FCBBF30074620
 FCBBF30075970
 55 FCBBF30076310//CAMP-DEPENDENT PROTEIN KINASE, BETA-CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C-BE-
 TA).//8.20E-166//240aa//100%//P22694
 FCBBF30078600
 FCBBF30079770

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FCBBF30080730//SPLICING FACTOR, ARGININE/SERINE-RICH 7 (SPLICING FACTOR 9G8).//3.40E-70//136aa//95%//Q16629
FCBBF30081000
FCBBF30085560//HYPOTHETICAL 60.3 KDA PROTEIN R13G10.2 IN CHROMOSOME III.//1.10E-87//531aa//38%//Q21988
5 FCBBF30088700
FCBBF30089380
FCBBF30091010
FCBBF30091520//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.70E-09//631aa//21%//P08640
10 FCBBF30093170//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.10E-63//173aa//65%//P51523
FCBBF30095410
FCBBF30099490
FCBBF30100080//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//1.10E-57//108aa//100%//Q99418
15 FCBBF30100120//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.//2.10E-192%//769aa//50%//AF127084
FCBBF30100410//Mus musculus testis-specific Y-encoded-like protein (Tspyl) mRNA, complete cds.//1.90E-56//324aa//42%//AF042180
20 FCBBF30101240
FCBBF30101300
FCBBF30105080
FCBBF30105440//Rattus norvegicus ion transporter protein (NRITP) mRNA, partial cds.//3.40E-36//82aa//91%//AF184921
25 FCBBF30105860//microtubule associated-protein orbit [Drosophila melanogaster].//1.00E-79//556aa//33%//BAA94248
FCBBF30106950
FCBBF30107290//MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (EC 3. 4. 24. 64) (ALPHA-MPP) (P-55) (HA1523) (KIAA0123).//1.00E-91//172aa//100%//Q10713
30 FCBBF30107330
FCBBF30114180
FCBBF30114850//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//3.20E-24//249aa//34%//AF159567
FCBBF30115230
35 FCBBF30115920//Homo sapiens nolp mRNA, complete cds.//9.40E-220//257aa//100%//AB017800
FCBBF30118670//Homo sapiens disintegrin and metalloproteinase domain 19 (ADAM19) mRNA, partial cds.//0//601aa//97%//AF134707
FCBBF30118890//Drosophila melanogaster La related protein (Iarp) mRNA, partial cds.//6.70E-25//221aa//35%//AF221108
40 FCBBF30125460
FCBBF30125880//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//6.40E-81//96aa//100%//AF125182
FCBBF30128420
45 FCBBF30129010//ZINC FINGER PROTEIN 36 (ZINC FINGER PROTEIN KOX18) (FRAGMENT).//1.20E-179//322aa//100%//P17029
FCBBF30130410//CALDESMON (CDM).//3.30E-06//170aa//32%//P12957
FCBBF30130580
FCBBF30132050//Homo sapiens mRNA for UDP-galactose:2-acetamido-2-deoxy-D-glucose3beta-galactosyltransferase.//2.10E-43//253aa//36%//Y15014
50 FCBBF30132660//Drosophila melanogaster Canton S tartan protein (trn) mRNA, complete cds.//2.00E-15//293aa//30%//U02078
FCBBF30135890//GLUTENIN, LOW MOLECULAR WEIGHT SUBUNIT PRECURSOR.//2.60E-07//163aa//34%//P10385
FCBBF30136230//NIL-2-A ZINC FINGER PROTEIN (NEGATIVE REGULATOR OF IL2) (TRANSCRIPTION FACTOR 8).//0//1090aa//94%//P37275
55 FCBBF30138000//trg protein - rat//1.30E-82//560aa//37%//I60486
FCBBF30142290//dJ127B20.3 (novel PHD finger protein) [Homo Sapiens].//1.00E-140//287aa//96%//CAB62994
FCBBF30143550//FYVE FINGER-CONTAINING PHOSPHOINOSITIDE KINASE (EC 2.7.1.68) (1-PHOSPHATIDYLI-

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NOSITOL-4-PHOSPHATE KINASE) (PIP5K) (PTDINS(4)P-5- KINASE) (P235).//0//1027aa//91%//Q9Z1T6
 FCBBF30145670
 FCBBF30151190
 FCBBF30153170//6-PHOSPHOFRUCTOKINASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1)
 5 (PHOSPHOHEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME B).//0//670aa//99%//P17858
 FCBBF30157270//Rattus norvegicus PAPIN mRNA, complete cds.//1.20E-179//639aa//58%//AF169411
 FCBBF30161780
 FCBBF30164510//RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).//0//794aa//98%//P55283
 FCBBF30166220//SERINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC (EC 2.1.2.1) (SERINE METHYLASE)
 10 (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT).//2.70E-12//33aa//100%//P34896
 FCBBF30169280//Petunia x hybrida GPGD14 (GPGD14) mRNA, complete cds.//1.40E-62//261aa//42%//AF049930
 FCBBF30169870
 FCBBF30170710
 FCBBF30171230//NEUROENDOCRINE CONVERTASE 2 PRECURSOR (EC 3.4.21.94) (NEC 2) (PC2) (PROHORMONE
 15 CONVERTASE 2) (PROPROTEIN CONVERTASE 2) (KEX2-LIKE ENDOPROTEASE 2).//1.70E-82//181aa//86%//P16519
 FCBBF30172330
 FCBBF30173960//erythroid differentiation-related factor 1 [Homo sapiens].//6.00E-32//113aa//100%//AAC00001
 FCBBF30175350//MITOGEN-ACTIVATED PROTEIN KINASE 7 (EC 2.7.1.-) (EXTRACELLULAR SIGNAL- REGULATED
 20 KINASE 5) (ERK5) (ERK4) (BMK1 KINASE).//4.60E-06//245aa//28%//Q13164
 FCBBF30177290//HYPOTHETICAL 47.6 KDA PROTEIN C16C10.5 IN CHROMOSOME III.//2.40E-28//133aa//46%//Q09251
 FCBBF30179180
 FCBBF30179740
 25 FCBBF30181730
 FCBBF30194370
 FCBBF30194550//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//9.90E-54//478aa//33%//P16157
 FCBBF30195690//SYNAPTOTAGMIN I.//1.30E-27//138aa//31%//P34693
 30 FCBBF30195700
 FCBBF30197840//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//0//869aa//91%//D64009
 FCBBF30198670//dof protein - fruit fly (Drosophila melanogaster).//6.60E-05//272aa//24%//T13712
 FCBBF30201630//Chlamydomonas reinhardtii dhc1 gene for 1-alpha dynein heavy chain.//1.10E-121//384aa//5896//
 35 AJ243806
 FCBBF30212210
 FCBBF30215240//mitogen inducible gene mig-2 - human.//2.20E-135//263aa//96%//S69890
 FCBBF30220950//OXISTEROLS RECEPTOR LXR-BETA (LIVER X RECEPTOR BETA) (NUCLEAR ORPHAN RECEPTOR
 40 LXR-BETA) (UBIQUITOUSLY-EXPRESSED NUCLEAR RECEPTOR) (NUCLEAR RECEPTOR NER).//6.90E-96//167aa//100%//P55055
 FCBBF30222910//Mus musculus Rap2 interacting protein 8 (RPIP8) mRNA, complete cds.//4.70E-29//76aa//46%//U73941
 FCBBF30223110
 FCBBF30223210//PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX).//1.70E-72//179aa//76%//P51805
 45 FCBBF30225930
 FCBBF30228940//Homo sapiens zinc finger protein dp mRNA, complete cds.//2.60E-14//114aa//42%//AF153201
 FCBBF30230610
 FCBBF30236670//Homo sapiens DEAD-box protein abstrakt (ABS) mRNA, complete cds.//1.00E-128//276aa//91%//AF195417
 50 FCBBF30250980//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//3.20E-06//190aa//28%//O24076
 FCBBF30255680//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//1.80E-275//641aa//82%//AF053768
 FCBBF30257370//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1 (CDV-1 PROTEIN).//2.80E-169//355aa//92%//O35594
 55 FCBBF30259050//Mus musculus (clone pMLZ-1) zinc finger protein (Zfp) mRNA, 3' end of cds.//1.40E-241//499aa//83%//L36315
 FCBBF30260210//Drosophila melanogaster KISMET-L long isoform (kis) mRNA, complete cds.//3.90E-178//420aa//

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68%//AF215703
 FCBBF30260480//Mus musculus putative E1-E2 ATPase mRNA, partial cds.//1.80E-78//154aa//95%//AF156547
 FCBBF30263080//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.20E-33//107aa//58%//P51522
 FCBBF30266510
 5 FCBBF30271990//ANKYRIN 1 (ERYTHROCYTE ANKYRIN).//3.00E-43//419aa//33%//Q02357
 FCBBF30275590//dedicator of cyto-kinesis 1 [Homo Sapiens].//1.00E-138//791aa//37%//NP_001371
 FCBBF30282020//cca3 protein - rat//5.50E-249//492aa//94%//T31081
 FCBBF30285930//ZINC FINGER PROTEIN ZFP-1 (MKR1 PROTEIN).//5.70E-68//125aa//97%//P08042
 FCBBF30287940
 10 FCBBF40000610//late gestation lung 2 protein [Rattus norvegicus].//5.00E-86//178aa//94%//AAF44721
 FCBBF40001920
 FCBBF40005000
 FCBBF50000410
 FCBBF50000610
 15 FCBBF50001650//Homo sapiens JP3 mRNA for junctophilin type3, complete cds.//1.20E-111//407aa//57%//AB042636
 FCBBF50003530//H.sapiens mRNA for dinG gene.//2.70E-137//181aa//100%//Y10571
 FCBBF50004950
 FEBRA20005040//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.90E-13//479aa//23%//P24733
 FEBRA20007820//MLN 64 PROTEIN (CAB1 PROTEIN).//7.00E-31//129aa//51%//Q14849
 20 FEBRA20018670
 FEBRA20026820//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-135//431aa//50%//Q05481
 FEBRA20027070//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.00E-139//333aa//70%//P51814
 FEBRA20029620
 25 FEBRA20031000//TRICHOHYALIN.//2.20E-16//360aa//26%//P37709
 FEBRA20031150//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.//2.00E-29//63aa//100%//AF226053
 FEBRA20031280
 FEBRA20031810
 FEBRA20035200
 30 FEBRA20035240//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//7.30E-05//108aa//31%//Q15427
 FEBRA20038220//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.50E-05//256aa//24%//P08640
 FEBRA20038330
 35 FEBRA20038970//Homo sapiens mRNA for stabilin-1 (stab1 gene).//1.30E-242//413aa//99%//AJ275213
 FEBRA20039070
 FEBRA20039260//NonF [Streptomyces griseus subsp. griseus].//2.20E-16//140aa//38%//AAD37457
 FEBRA20040230
 FEBRA20040260
 40 FEBRA20040290
 FEBRA20040560//Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA, complete cds.//1.70E-112//204aa//100%//AF134404
 FEBRA20045380//EVI-5 homolog [Homo sapiens].//7.00E-49//130aa//81%//AAC16031
 FEBRA20046200//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//1.70E-25//368aa//30%//Q01484
 45 FEBRA20046280
 FEBRA20046510//ZINC FINGER PROTEIN 135.//1.10E-94//260aa//62%//P52742
 FEBRA20057010//ZINC FINGER PROTEIN 195.//1.30E-12//47aa//70%//014628
 FEBRA20063720//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//3.10E-243//586aa//73%//Q03923
 50 FEBRA20076200
 FEBRA20078180
 FEBRA20078800//NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).//2.30E-96//192aa//96%//075251
 55 FEBRA20080860
 FEBRA20082660
 FEBRA20083410
 FEBRA20084750

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FEBRA20086600
 FEBRA20087550//damage-specific DNA binding protein 2 (48kD) [Homo sapiens]//1.10E-106//119aa//94%//NP_000098
 FEBRA20088610//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP)//2.40E-14//145aa//30%//P10123
 5 FEBRA20088810//FIBROBL GROWTH FACTOR-17 PRECURSOR (FGF-17)//1.00E-102//193aa//99%//060258
 FEBRA20090160//MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (EC 2.7.1.-) (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)//1.10E-15//111aa//48%//Q02779
 FEBRA20090220//TRANSLATION INITIATION FACTOR EIF-2B EPSILON SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)//0//721aa//90%//P47823
 10 FEBRA20091620
 FEBRA20092760//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN)//2.50E-81//165aa//80%//P48059
 FEBRA20093270
 FEBRA20093280
 15 FEBRA20095410
 FEBRA20098040
 FEBRA20099860//dynactin 3 (p22); dynactin light chain [Homo Sapiens]//1.70E-41//89aa//100%//NP_009165
 FEBRA20101410
 FEBRA20108020
 20 FEBRA20108580
 FEBRA20115930
 FEBRA20116650
 FEBRA20121200
 FEBRA20121950//X INACTIVE SPECIFIC TRANSCRIPT PROTEIN (FRAGMENT)//1.60E-07//155aa//24%//P27571
 25 FEBRA20141980
 FEBRA20150420//HYPOTHETICAL 131.5 KDA PROTEIN CO2F12.7 IN CHROMOSOME X//6.90E-56//877aa//24%//Q11102
 FEBRA20151750//Mus musculus (clone E5.53) Huntington disease (hdh) gene, exon 5//2.60E-12//88aa//43%//L34024
 30 FEBRA20163980
 FEBRA20170240//ZINC FINGER PROTEIN 75//7.90E-158//278aa//99%//P51815
 FEBRA20172230//Mus musculus schwannoma-associated protein (SAM9) mRNA, complete cds//1.70E-57//295aa//40%//AF026124
 FEBRA20173330//PROTEIN KINASE CLK3 (EC 2.7.1.-)//4.80E-277//490aa//99%//P49761
 35 FEBRA20175020
 FEBRA20175330
 FEBRA20177800//RNA binding motif protein 9 [Homo sapiens]//4.00E-09//75aa//95%//NP_055124
 FEBRA20180510
 FEBRA20182030
 40 FEBRA20187460
 FEBRA20191720//REGULATOR OF G-PROTEIN SIGNALING 11 (RGS11)//2.00E-73//104aa//100%//094810
 HCHON10000150//SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1)//4.10E-74//154aa//84%//Q13642
 HCHON10001660
 45 HCHON20000870//SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37)//2.10E-21//300aa//26%//Q05609
 HCHON20002650//EARLY GROWTH RESPONSE PROTEIN 2 (EGR-2) (KROX-20 PROTEIN)//9.90E-05//166aa//26%//P51774
 HCHON20002710//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 13 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 13) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 13)//7.40E-10//114aa//28%//P38187
 50 HCHON20015050//LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X)//8.60E-06//250aa//26%//P20702
 HEART10001420//Mus musculus skm-BOP1 (Bop) mRNA, complete cds//6.10E-259//485aa//94%//U76373
 HEART10001490//ACTIN INTERACTING PROTEIN 2//1.80E-71//243aa//58%//P46681
 55 HEART20009590//Homo sapiens mRNA for paraplegin-like protein//7.10E-47//145aa//67%//Y18314
 HEART20019310//Mus musculus RING-finger protein MURF mRNA, complete cds//6.70E-118//362aa//61%//AF294790
 HEART20022200//METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE M 2) (INITIATION

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FACTOR 2 ASSOCIATED 67 KDA GLYCOPROTEIN) (P67).//1.50E-209//447aa//86%//P50579
HEART20031680
HEART20047640//CALCIUM/CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
1C (EC 3.1.4.17) (CAM-PDE 1C).//0//769aa//94%//Q63421
5 HEART20063100//H. sapiens mRNA histone RNA hairpin-binding protein.//5.60E-114//212aa//100%//Z71188
HEART20082570//AMINOMETHYLTRANSFERASE PRECURSOR (EC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM T
PROTEIN).//5.50E-113//210aa//69%//P28337
HHDPC10001140
HHDPC20051850//STEROID RECEPTOR PROTEIN DG6.//9.50E-43//101aa//89%//015173
10 HHDPC20081230//NUCL (PROTEIN C23).//0//681aa//92%//P19338
HHDPC20082790
HHDPC20082970
HHDPC20088160
HLUNG20008460//DIAPHANOUS PROTEIN HOMOLOG 2.//7.60E-33//521aa//26%//060879
15 HLUNG20009260
HLUNG20009550
HLUNG20010130
HLUNG20011260//TYROSINE-PROTEIN KINASE SRC-1 (EC 2.7.1.112) (P60-SRC-1).//1.10E-46//92aa//100%//
P13115
20 HLUNG20011440
HLUNG20011460//Rattus norvegicus serine-arginine-rich splicing regulatory protein SRRP86 mRNA, complete cds.//
1.20E-159//398aa//79%//AF234765
HLUNG20012140
HLUNG20014590//ZINC FINGER PROTEIN 135.//1.20E-122//350aa//59%//P52742
25 HLUNG20015070//SLIT PROTEIN PRECURSOR.//5.00E-14//167aa//33%//P24014
HLUNG20015180//BALBIANI RING PROTEIN 3 PRECURSOR.//8.80E-08//444aa//24%//Q03376
HLUNG20020500
HLUNG20020850//TLM PROTEIN (TLM ONCOGENE).//5.00E-17//91aa//54%//P17408
HLUNG20021450
30 HLUNG20023030
HLUNG20024050
HLUNG20025620
HLUNG20028110//zinc finger protein - fission yeast (Schizosaccharomyces pombe).//2.70E-23//140aa//38%//T39456
HLUNG20029420
35 HLUNG20029490
HLUNG20030420//Mus musculus mRNA for MAIL, complete cds.//1.00E-164//728aa//68%//AB020974
HLUNG20030490//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//1.70E-64//335aa//42%//AF047465
HLUNG20030610
HLUNG20031620
40 HLUNG20032460//LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOX-
YPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOX-
YPEPTIDASE C).//8.60E-274//440aa//99%//P42785
HLUNG20033060//Homo sapiens GAP-like protein (N61) mRNA, complete cds.//1.20E-81//389aa//45%//AF251038
HLUNG20033310
45 HLUNG20033350
HLUNG20034970
HLUNG20037140
HLUNG20037160//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.90E-131//439aa//54%//P10267
HLUNG20037780
50 HLUNG20038330
HLUNG20041540//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.80E-08//286aa//24%//P08640
HLUNG20041590//ubiquitous tetratricopeptide containing protein RoXaN [Homo sapiens].//1.00E-158//737aa//42%//
AAF05541
55 HLUNG20042730//CYTOCHROME P450 4A4 (EC 1.14.14.1) (CYP1A4) (PROSTAGLANDIN OMEGA- HYDROXY-
LASE) (P450-P-2).//4.90E-126//442aa//49%//P10611
HLUNG20045340//MOB2 PROTEIN (MPS1 BINDER 2).//4.60E-27//135aa//37%//P43563
HLUNG20047070

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HLUNG20050760
 HLUNG20051330
 HLUNG20052300//AIG1 PROTEIN.//3.00E-23//216aa//30%//P54120
 HLUNG20054790//PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT (EC 2.7.1.137) (IB PI3-KINASE
 5 P101 SUBUNIT) (PTDINS-3-KINASE P101) (PI3K) (P101-PI3K).//8.30E-22//292aa//25%//002696
 HLUNG20055240
 HLUNG20056560
 HLUNG20057380
 HLUNG20059240
 10 HLUNG20060670
 HLUNG20063700//H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA.//3.60E-22//62aa//79%//Z35278
 HLUNG20065700
 HLUNG20065990//SYNTAXIN 4.//8.80E-127//267aa//96%//Q12846
 HLUNG20067810
 15 HLUNG20068120//NUCLEAR TRANSITION PROTEIN 2 (TP-2).//7.10E-06//86aa//38%//P11101
 HLUNG20069350//CALCYPHOSINE.//1.80E-13//128aa//31%//Q13938
 HLUNG20070410
 HLUNG20072100//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds.//1.40E-236//404aa//79%//AF198349
 HLUNG20072190
 20 HLUNG20072450
 HLUNG2007433Q
 HLUNG20079310
 HLUNG20081390//DNAJ PROTEIN.//1.60E-17//98aa//47%//P35515
 HLUNG20081530//NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NF-H).//
 25 1.90E-09//220aa//25%//P12036
 HLUNG20082350//Homo sapiens goodpasture antigen-binding protein (COL4A3BP) mRNA, complete cds.//0//399aa//
 93%//AF136450
 HLUNG20083330//alpha (III) collagen [Homo Sapiens]//5.40E-61//113aa//99%//CAA29886
 HLUNG20083480//Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52.//9.00E-178//527aa//68%//
 30 D82364
 HLUNG20083840
 HLUNG20083960
 HLUNG20084790//HYPOTHETICAL 65.2 KDA TRP-ASP REPEATS CONTAINING PROTEIN D2030.9 IN CHROMO-
 SOME 1.//5.50E-47//161aa//53%//P90794
 35 HLUNG20085210//Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds.//9.60E-28//162aa//95%//AF248540
 HLUNG20088750
 HLUNG20092530
 HLUNG20093030
 HLUNG20094130
 40 KIDNE20011600
 KIDNE20016360//Rattus norvegicus potassium channel (erg2) mRNA, complete cds.//0//418aa//96%//AF016192
 KIDNE20024380
 KIDNE20027980
 KIDNE20080690//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-) //5.80E-114//445aa//48%//P91408
 45 KIDNE20081170//Homo sapiens microtubule-based motor (HsKIFC3) mRNA, complete cds.//6.20E-153//216aa//
 99%//AF004426
 KIDNE20083150
 KIDNE20083620//L-ASPARAGINASE (EC 3.5.1.1) (L-ASPARAGINE AMIDOHYDROLASE).//2.60E-53//148aa//43%//
 Q9ZSD6
 50 KIDNE20084030
 KIDNE20084040//PHOSPHOLIPASE D1 (EC 3.1.4.4) (PLD 1) (CHOLINE PHOSPHATASE 1) (PHOSPHATIDYLCHO-
 LINE-HYDROLYZING PHOSPHOLIPASE D1).//3.30E-70//134aa//100%//Q13393
 KIDNE20084730//Homo sapiens FH1/FH2 domain-containing protein FHOS (FHOS) mRNA, complete cds.//2.60E-
 148//599aa//52%//AF113615
 55 KIDNE20084800
 KIDNE20086490
 KIDNE20086660
 KIDNE20086970

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KIDNE20087880
KIDNE20088240//atopy related autoantigen CALC [Homo sapiens]//1.00E-26//300aa//26%//CAA76830
KIDNE20089870//HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA-BINDING PROTEIN 7)//4.30E-237//422aa//99%//Q16576
5 KIDNE20091090
KIDNE20094260
KIDNE20094670//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.10E-124//399aa//59%//AF227209
KIDNE20095530
10 KIDNE20133460//Homo sapiens mRNA for sperm protein.//3.40E-146//284aa//100%//X91879
KIDNE20133880
KIDNE20134130
KIDNE20134890//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//7.70E-05//169aa//21%//Q02224
KIDNE20137310
15 KIDNE20138450
KIDNE20140870//zinc finger protein 106 [Mus musculus]//2.10E-288//822aa//67%//AF060246
KIDNE20141120
KIDNE20141700//40S RIBOSOMAL PROTEIN S4, X ISOFORM (SINGLE COPY ABUNDANT MRNA PROTEIN) (SCR10)//2.60E-72//153aa//89%//P12750
20 KIDNE20142680
KIDNE20142900//THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN)//1.80E-71//119aa//100%//P07204
KIDNE20143200
KIDNE20147170//acetylglutamate synthase - fission yeast (Schizosaccharomyces pombe)//8.40E-15//143aa//37%//T40666
25 KIDNE20148080
KIDNE20149780//NG28 [Mus musculus]//3.50E-66//367aa//44%//AAC97966
KIDNE20150730//REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1)//2.40E-06//84aa//41%//P49646
KIDNE20152440//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds.//1.80E-181//388aa//93%//D87258
30 KIDNE20154330//Rattus norvegicus mRNA for multi PDZ domain protein.//0//763aa//87%//AJ001320
KIDNE20154830
KIDNE20155980
KIDNE20157100
35 KIDNE20160360//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR)//7.10E-40//194aa//41%//Q99418
KIDNE20160960
KIDNE20163710
KIDNE20165390//Homo sapiens mRNA for beta-tubulin folding cofactor D.//0//709aa//94%//AJ006417
40 KIDNE20169180//UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)//0//615aa//99%//P07911
KIDNE20170400
KIDNE20173150//Bos taurus mRNA for mitochondrial aralkyl acylCoA:amino acid N-acyltransferase.//2.90E-53//277aa//40%//AJ223301
45 KIDNE20173430//Homo sapiens PDZ domain containing-protein (PDZK1) mRNA, complete cds.//7.90E-28//150aa//34%//AF012281
KIDNE20176030
KIDNE20181670
KIDNE20182540
50 KIDNE20186170//UDP-GLUCURONOSYLTRANSFERASE 2B13 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UD-PGT) (EGT10)//4.40E-38//214aa//39%//P36512
KIDNE20188630
KIDNE20189890//Homo sapiens mRNA for KARP-1-binding protein 2 (KAB2), complete cds.//6.00E-30//177aa//44%//AB022658
55 KIDNE20189960//TREHALASE PRECURSOR (EC 3.2.1.28) (ALPHA, ALPHA-TREHALASE) (ALPHA, ALPHA-TREHALOSE GLUCOHYDROLASE)//1.40E-224//421aa//97%//043280
KIDNE20191870
LIVER20006260//Mus musculus zinc finger protein ZFP113 mRNA, complete cds.//4.50E-183//385aa//8596//

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- AF167320
LIVER20007690
LIVER20007750
LIVER20010510
- 5 LIVER20010760//Homo sapiens C-type lectin-like receptor-1 mRNA, complete cds.//3, 10E-134//208aa//100%//AF200949
LIVER20010990//Rattus norvegicus mRNA for putative integral membrane transport protein (UST1r).//7.00E-52//196aa//54%//Y09945
LIVER20011640//Human proline rich calmodulin-dependent protein kinase mRNA, complete cds.//2.00E-116//221aa//97%//U23460
- 10 LIVER20013890
LIVER20026440//CYTOCHROME P450 4F3 (EC 1.14.13.30) (CYP1B3) (LEUKOTRIENE-B4 OMEGA- HYDROXY-LASE) (LEUKOTRIENE-B4 20-MONOOXYGENASE) (CYTOCHROME P450- LTB-OMEGA).//2.60E-136//295aa//84%//Q08477
- 15 LIVER20030650//WHITE PROTEIN.//7.20E-09//229aa//25%//Q05360
LIVER20032340
LIVER20038000//MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN (CARNITINE/ACYLCARNITINE TRANSLOCASE) (CAC).//9.40E-40//148aa//38%//P97521
LIVER20040740//RETINAL-BINDING PROTEIN (RALBP).//3.10E-60//337aa//37%//P49193
- 20 LIVER20055270//SELENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2).//2.70E-204//376aa//97%//Q99611
MESAN20006200//ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV).//1.70E-84//174aa//95%//P07355
MESAN20007110
- 25 MESAN20008150
MESAN20008940
MESAN20009090//Homo sapiens CEGP1 protein (CEGP1), mRNA//1.10E-179//553aa//58%//NM_020974
MESAN20016270//ZINC FINGER PROTEIN 37A (ZINC FINGER PROTEIN KOX21) (FRAGMENT).//1.60E-141//242aa//100%//P17032
- 30 MESAN20021130//Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds.//8.20E-168//346aa//91%//U07747
MESAN20021220//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS).//7.40E-26//197aa//30%//002833
MESAN20021470//SPINDLIN (30000 MR METAPHASE COMPLEX) (SSEC P).//3.50E-123//229aa//98%//Q61142
- 35 MESAN20021860
MESAN20026870
MESAN20027240//Rho guanine nucleotide exchange factor (GEF) 10 [Homo sapiens].//1.00E-134//620aa//40%//NP_055444
MESAN20027900//COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR//0//1001aa//98%//P12111
- 40 MESAN20029780
MESAN20030350//Mus musculus diaphanous-related formin (Dia2) mRNA, complete cds.//6.60E-301//669aa//84%//AF094519
MESAN20030370
MESAN20030390
- 45 MESAN20033220//ALDEHYDE DEHYDROGENASE 7 (EC 1.2.1.5).//1.60E-24//54aa//100%//P43353
MESAN20034440//39.1 KDA PROTEIN IN SURE-CYSC INTERGENIC REGION.//2.70E-07//117aa//31%//Q57261
MESAN20038520//DNA-DIRECTED RNA POLYMERASE III 128 KDA POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//0//831aa//70%//P25167
MESAN20041380
- 50 MESAN20045750
MESAN20056890//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KDA) (PR264 PROTEIN).//3.30E-12//97aa//48%//Q01130
MESAN20057240//DNA EXCISION REPAIR PROTEIN ERCC-1.//5.90E-120//195aa//9896//P07992
MESAN20058110//65 KDA FK506-BINDING PROTEIN PRECURSOR (EC 5.2.1.8) (FKBP65) (FKBPRP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) (IMMUNOPHILIN FKBP65).//8.00E-117//229aa//89%//Q61576
- 55 MESAN20059570//Rattus norvegicus mRNA for seven transmembrane receptor, complete cds.//1.00E-173//484aa//63%//BAA82518

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MESAN20060220
MESAN20060430
MESAN20065990//Human protein serine/threonine kinase stk2 mRNA, complete cds.//2.40E-07//65aa//50%//L20321
MESAN20067430//TROPOMYOSIN, FIBROBLAST ISOFORM TM3.//1.80E-39//87aa//100%//P09494
5 MESAN20069530//LIM domain only 7 isoform c [Homo Sapiens]//2.20E-286//545aa//99%//NP_056667
MESAN20084150//Mus musculus secretory carrier membrane protein 4 mRNA, complete cds.//2.20E-48//128aa//72%//AF224721
MESAN20085360
MESAN20089260
10 MESAN20090190//CEGP1 protein [Homo sapiens].//0//880aa//57%//NP_066025
MESAN20094180
MESAN20095220
MESAN20095800//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//1.60E-31//150aa//46%//P52017
15 NESOP20004520//LYMPHOCYTE-SPECIFIC PROTEIN LSP1 (PP52 PROTEIN) (52 KDA PHOSPHOPROTEIN) (LYMPHOCYTE-SPECIFIC ANTIGEN WP34).//3.40E-173//321aa//99%//P33241
NESOP20005040
NT2NE20018740
NT2NE20018890//Homo sapiens WD-repeat protein 6 (WDR6) mRNA, complete cds.//6.60E-184//257aa//99%//AF099100
20 NT2NE20021860//Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds.//9.00E-68//466aa//36%//AF287478
NT2NE20026200//TRANSKETOLASE (EC 2.2.1.1) (TK).//1.80E-160//310aa//99%//P29401
NT2NE20026510//basic protein, cytosolic - fruit fly (Drosophila melanogaster)//6.10E-35//202aa//41%//S47857
25 NT2NE20028700
NT2NE20033150
NT2NE20037050//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KDA SUBUNIT RELATED-PROTEIN 2.//7.20E-08//109aa//38%//Q15696
NT2NE20038870//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//5.90E-153//405aa//72%//P98168
30 NT2NE20039210
NT2NE20042550//ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).//7.80E-15//153aa//28%//P43188
NT2NE20045190
NT2NE20047870
35 NT2NE20053230
NT2NE20053950//ZINC FINGER PROTEIN 136.//6.40E-108//284aa//64%//P52737
NT2NE20059210
NT2NE20059680//Homo sapiens integrin cytoplasmic domain associated protein (Icap-1a) mRNA, complete cds.//1.80E-44//96aa//100%//AF012023
40 NT2NE20060750//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.20E-69//198aa//68%//P16415
NT2NE20061030//ZINC FINGER PROTEIN 165.//3.00E-39//125aa//65%//P49910
NT2NE20062880
NT2NE20064780//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.10E-05//443aa//24%//P32323
NT2NE20066590
45 NT2NE20069580
NT2NE20070520
NT2NE20073650
NT2NE20077250//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//1.20E-173//349aa//94%//AF011792
50 NT2NE20077270
NT2NE20077860
NT2NE20079670//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.60E-98//345aa//47%//P51523
NT2NE20080770
NT2NE20082130
55 NT2NE20082600//Homo sapiens zinc finger protein dp mRNA, complete cds.//2.10E-19//163aa//42%//AF153201
NT2NE20086070
NT2NE20087270//Homo sapiens putative RNA binding protein mRNA, alternatively spliced, complete cds.//4.30E-14//221aa//29%//AF119121

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NT2NE20087850//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT)//1.80E-08//75aa//40%//P40603
 NT2NE20088030
 NT2NE20092950
 5 NT2NE20095230//Homo sapiens HSKM-B (HSKM-B) mRNA, complete cds.//1.40E-09//112aa//32%//AF226053
 NT2NE20104000
 NT2NE20107810
 NT2NE20108420//KES1 PROTEIN.//4.70E-25//312aa//31%//P35844
 NT2NE20111190//C-TERMINAL BINDING PROTEIN 2.//9.00E-54//137aa//84%//P56545
 10 NT2NE20112210
 NT2NE20114850
 NT2NE20117580//NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).//1.20E-76//153aa//9596//075251
 NT2NE20119980//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//6.10E-48//135aa//74%//Q13829
 15 NT2NE20123610
 NT2NE20124570
 NT2NE20126030
 NT2NE20127900//Homo sapiens myo-inositol 1-phosphate synthase A1 (ISYNA1) mRNA, complete cds.//1.40E-269//465aa//99%//AF220530
 20 NT2NE20140130//SEMAPHORIN 3B PRECURSOR (SEMAPHORIN V) (SEMA V).//1.90E-42//90aa//100%//Q13214
 NT2NE20140280
 NT2NE20141040//DOWN SYNDROME CRITICAL REGION PROTEIN 1.//1.80E-105//197aa//99%//P53805
 NT2NE20145250//SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN).//2.50E-58//141aa//88%//P55821
 25 NT2NE20146510//HYPOTHETICAL 104.7 KDA PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR.//6.20E-08//179aa//23%//P46504
 NT2NE20148690
 NT2NE20149500
 30 NT2NE20150610
 NT2NE20152620
 NT2NE20153620//mitogen inducible gene mig-2 - human//7.90E-147//449aa//63%//S69890
 NT2NE20155650//RETROVIRUS-RELATED ENV POLYPROTEIN.//2.30E-29//114aa//33%//P10267
 NT2NE20157120
 35 NT2NE20165190
 NT2NE20167660//Mus musculus nuclear localization signal binding protein (spot-1) mRNA, complete cds.//3.50E-09//76aa//40%//S79410
 NT2NE20173970//Rattus norvegicus beta-catenin binding protein mRNA, complete cds.//1.60E-24//134aa//46%//AF169825
 40 NT2NE20177210//Leishmania major partial ppg1 gene for proteophosphoglycan.//1.10E-06//169aa//27%//AJ243460
 NT2NE20181760
 NT2NE20181800
 NT2NE20184720
 NT2RI20016240
 45 NT2RI20021200
 NT2RI20033920
 NT2RI20093010//BIFUNCTIONAL METHYLENETETRAHYDROFOLATE DEHYDROGENASE/CYCLOHYDROLASE, MITOCHONDRIAL PRECURSOR [INCLUDES: NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15); METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9)].//5.90E-34//86aa//81%//P13995
 50 NT2RP70001120//GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (GABPB1).//2.50E-113//384aa//62%//Q00420
 NT2RP70001730//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//4.30E-249//589aa//74%//U65079
 55 NT2RP70003110//ELASTIN PRECURSOR (TROPOELASTIN).//1.40E-165//613aa//61%//P15502
 NT2RP70012830//CALPHOTIN.//7.90E-17//445aa//28%//Q02910
 NT2RP70022820
 NT2RP70027790//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.80E-23//186aa//34%//

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Q01730
 NT2RP70029780//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.30E-118//381aa//56%//P16415
 NT2RP70030840//Mus musculus schlafen3 (S1fn3) mRNA, complete cds.//3.70E-55//328aa//33%//AF099974
 NT2RP70031070//36 KDA NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//
 5 1.20E-23//169aa//34%//Q61672
 NT2RP70031340
 NT2RP70031480
 NT2RP70035110//Caenorhabditis elegans UNC-89 (unc-89) gene, complete cds.//1.50E-07//229aa//26%//U33058
 NT2RP70046410//BASONUCLIN.//3.60E-71//318aa//43%//Q01954
 10 NT2RP70049610
 NT2RP70056290
 NT2RP70056690//F-SPONDIN PRECURSOR.//2.20E-15//366aa//24%//P35447
 NT2RP70057500//Hypothetical zinc finger-like protein [Homo sapiens].//0//799aa//94%//AAF88107
 NT2RP70064570//CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL
 15 PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3
 LARGE SUBUNIT).//9.40E-86//278aa//40%//Q64691
 NT2RP70074800
 NT2RP70075300//ZINC FINGER PROTEIN 211 (ZINC FINGER PROTEIN C2H2-25).//9.60E-121//333aa//63%//
 Q13398
 20 NT2RP70075800//HYPOTHETICAL 43.1 KDA TRP-ASP REPEATS CONTAINING PROTEIN K04G11.4 IN CHRO-
 MOSOME X.//1.80E-13//244aa//25%//Q93847
 NT2RP70080150
 NT2RP70084540
 NT2RP70087140//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.40E-11//264aa//31%//
 25 P17437
 NT2RP70090870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//4.20E-230//592aa//61%//
 Q05481
 NTONG20002230//Mus musculus RW1 protein mRNA, complete cds.//5.20E-97//546aa//34%//AF060565
 NTONG20005310
 30 NTONG20017620
 NTONG20029850//CALCYPHOSINE (R2D5 ANTIGEN).//1.60E-24//183aa//32%//P41150
 NTONG20031580//heat shock 27kD protein family, member 7 (cardiovascular); cardiovascular heat shock protein [Ho-
 mo sapiens].//6.10E-69//141aa//95%//NP_055239
 NTONG20032100//KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13).//4.20E-175//351aa//
 35 96%//P13646
 NTONG20034540//CGMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3. 1. 4. 17) (CYCLIC GMP
 STIMULATED PHOSPHODIESTERASE) (CGS-PDE).//0//713aa//99%//000408
 NTONG20035150//RING CANAL PROTEIN (KELCH PROTEIN).//9.10E-30//570aa//25%//Q04652
 NTONG20043080//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC
 40 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//4.30E-12//226aa//28%//P11799
 NTONG20048440//P116 RHO-INTERACTING PROTEIN (P116RIP) (RIP3).//1.60E-269//588aa//87%//P97434
 NTONG20049180
 NTONG20053630//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.30E-12//247aa//29%//P08640
 45 NTONG20053730//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
 RASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//8.70E-
 104//340aa//60%//Q24574
 NTONG20053910//Bos taurus differentiation enhancing factor 1 (DEF-1) mRNA, complete cds.//2.50E-198//891aa//
 4596//AF112886
 50 NTONG20055200//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//1.10E-269//522aa//
 83%//Q07803
 NTONG20058010//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVAT-
 ING ENZYME).//3.90E-124//398aa//54%//068040
 NTONG20058220//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//8.60E-14//349aa//25%//AF153085
 55 OCBBF20000740//Homo sapiens mRNA for ISLR, complete cds.//3.60E-87//287aa//59%//AB003184
 OCBBF20001780
 OCBBF20005220//Rattus norvegicus Fos-related antigen mRNA, complete cds.//3.40E-233//552aa//84%//U34932
 OCBBF20009820

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OCBBF20011860//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.//4.30E-33//98aa//66%//AF307844

OCBBF20012520//Homo sapiens mRNA for ISLR, complete cds.//6.50E-88//287aa//59%//AB003184

OCBBF20016390

5 OCBBF20016810//enhancer of polycomb [Mus musculus]//0//743aa//92%//AF079765

OCBBF20109450

OCBBF20109780

OCBBF20110210//KILON PROTEIN PRECURSOR (KINDRED OF IGLON).//4.30E-182//352aa//94%//Q9Z0J8

OCBBF20110730

10 OCBBF20111370//BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 2.//5.70E-84//324aa//52%//054940

OCBBF20111600//69 KDA ISLET CELL AUTOANTIGEN (ICA69) (ISLET CELL AUTOANTIGEN 1).//1.30E-113//335aa//57%//Q05084

OCBBF20112280//Mesembryanthemum crystallinum phosphoenolpyruvate/phosphate translocator precursor (PPT) mRNA, complete cds.//7.00E-09//113aa//30%//AF223359

15 OCBBF20112320

OCBBF20113110

OCBBF20115360

OCBBF20116250//Mus musculus C2H2-type zinc finger protein (Evi9) mRNA, complete cds.//0//592aa//99%//AF051525

20 OCBBF20117220

OCBBF20118720

OCBBF20119810

OCBBF20120010//Homo sapiens zinc metalloprotease ADAMTS6 (ADAMTS6) mRNA, complete cds.//1.60E-44//217aa//42%//AF140674

25 OCBBF20120950//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//1.00E-28//201aa//34%//Q60821

OCBBF20121910//LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN).//0//740aa//98%//P51826

OCBBF20123200

30 OCBBF20142290

OCBBF20147070

OCBBF20152330

OCBBF20155030

OCBBF20156450//ZINC FINGER PROTEIN 75.//8.20E-163//289aa//99%//P51815

35 OCBBF20157970//ZINC FINGER PROTEIN 135.//2.80E-98//306aa//56%//P52742

OCBBF20160380//liver stage antigen LSA-1 - Plasmodium falciparum.//1.10E-21//938aa//24%//A45592

OCBBF20165900//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//4.80E-09//145aa//31%//P19467

OCBBF20165910//Mus musculus pecanex 1 mRNA, complete cds.//4.20E-116//407aa//53%//AF096286

OCBBF20166890//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//4.20E-21//124aa//45%//042184

40 OCBBF20166900//ZINC FINGER PROTEIN CLONE 647 (FRAGMENT).//9.00E-18//196aa//30%//P15622

OCBBF20167290//probable acyl-CoA dehydrogenase - Deinococcus radiodurans (strain R1).//2.50E-72//222aa//60%//D75616

OCBBF20170350//Mus musculus mRNA for GATS protein.//2.50E-56//121aa//96%//AJ296173

OCBBF20174580//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT).//7.10E-16//240aa//25%//P25012

45 OCBBF20174890//ankyrin 3, long splice form - human.//1.10E-150//178aa//100%//A55575

OCBBF20175360//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//3.80E-11//101aa//36%//AF159567

OCBBF20176650

50 OCBBF20177540//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//1.40E-110//223aa//86%//Q03309

OCBBF20177910

OCBBF20182060//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.20E-82//265aa//61%//U13152

OCBBF20185630

55 OCBBF20188280

OCBBF20191950//VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR).//0//720aa//97%//P98155

PANCR10000860//ELASTASE IIIB PRECURSOR (EC 3.4.21.70) (PROTEASE E).//1.10E-52//87aa//97%//P08861

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PEBLM10001470//glutamine (Q)-rich factor 1, QRF-1 [mice, B-cell leukemia, BCL1, Peptide Partial, 84 aa]//5.00E-42//84aa//98%//AAB29272

PEBLM20001800//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876

PEBLM20003260//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.90E-62//151aa//70%//P51522

5 PEBLM20005020

PLACE50001290//HYPOTHETICAL 87.9 KDA PROTEIN F44G.4.1 IN CHROMOSOME II PRECURSOR.//2.90E-16//102aa//43%//P54073

PLACE50001390

PLACE60001910

10 PLACE60004260//CYSTATIN M PRECURSOR (CYSTATIN E).//1.50E-37//81aa//97%//Q15828

PLACE60006300

PLACE60011180

PLACE60012620//LYSOSOMAL TRAFFICKING REGULATOR (BEIGE HOMOLOG).//8.40E-14//128aa//38%//Q99698

15 PLACE60017120

PLACE60052940//TRANSCRIPT REGULATORY PROTEIN GAL11.//1.70E-05//445aa//23%//P32257

PLACE60053280

PLACE60054230//DIAPHANOUS PROTEIN HOMOLOG 2.//1.00E-35//385aa//26%//O60879

PLACE60054820//HYPOTHETICAL PROTEIN KIAA0032.//1.20E-50//180aa//61%//Q15034

20 PLACE60054870//MYOSIN HEAVY CHAIN, NONMUS TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMM-HC-B).//3.70E-11//434aa//20%//P35580

PLACE60055350

PLACE60055460//Homo sapiens leucine-zipper protein FKSG13 (FKSG13) mRNA, complete cds.//5.40E-164//327aa//99%//AF312393

25 PLACE60055590//MYOSIN-BINDING PROTEIN H (MYBP-H) (H-PROTEIN) (86 KDA PROTEIN).//1.30E-05//124aa//35%//Q05623

PLACE60056910

PLACE60057860

PLACE60061370

30 PLACE60062660//ADP-ribosylation factor binding protein GGA1; ADP-ribosylation factor binding protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 1 [Homo sapiens].//6.00E-84//249aa//93%//NP_037497

PLACE60062870

PLACE60063940

PLACE60064180//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

35 HELICASE.//1.90E-51//368aa//37%//O22899

PLACE60064740//ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MCFP1).//4.80E-11//157aa//31%//Q25434

PLACE60066970//ZINC FINGER PROTEIN 191.//1.30E-36//115aa//48%//O14754

PLACE60068710//SUPPRESSOR PROTEIN SRP40.//9.50E-43//238aa//50%//P32583

40 PLACE60069880

PLACE60070500

PLACE60071800//CORONIN-LIKE PROTEIN P57.//3.80E-60//108aa//81%//Q92176

PLACE60072390

PLACE60072420

45 PLACE60073090//Homo sapiens myo-inositol 1-phosphate synthase A1 (ISYNA1) mRNA, complete cds.//6.60E-219//362aa//98%//AF220530

PLACE60074820

PLACE60077870

PLACE60080360//mucin [Homo sapiens].//5.50E-05//164aa//30%//CAA84032

50 PLACE60081260

PLACE60082850

PLACE60087680//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3).//2.30E-103//255aa//79%//P17936

PLACE60088240

55 PLACE60092280

PLACE60092370

PLACE60093380

PLACE60095240

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PLACE60095600//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.70E-28//201aa//38%//Q09475
 PLACE60098350//Human hepatocellular carcinoma associated protein (JCL-1) mRNA, complete cds.//5.20E-285//
 558aa//97%//U92544
 PLACE60104630//macrophage migration inhibitory factor (glycosylation-inhibiting factor) [Homo sapiens]//9.70E-51//
 5 110aa//93%//XP_000858
 PLACE60105680//Homo sapiens mRNA for TU12B1-TY, complete cds.//1.70E-30//65aa//64%//AB032773
 PLACE60107010//SUPPRESSOR PROTEIN SRP40.//3.80E-05//117aa//29%//P32583
 PLACE60109910
 PLACE60113340//BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
 10 PRECURSOR (HSPG) (PERLECAN) (PLC).//5.90E-65//238aa//32%//Q05793
 PLACE60118810//Rattus norvegicus kinesin light chain KLCt mRNA, complete cds.//1.90E-230//504aa//87%//
 AF166267
 PLACE60119700//Homo sapiens mRNA for ABP32, complete cds.//2.30E-21//47aa//100%//AB018357
 PLACE60120280//SER/THR-RICH PROTEIN T10 IN DGCR REGION.//6.00E-99//126aa//84%//P54797
 15 PLACE60122970//novel C2H2 type zinc finger protein//5.60E-84//169aa//98%//CAC10457
 PLACE60132200//TRICHOHYALIN.//3.10E-47//297aa//47%//P37709
 PLACE60132320
 PLACE60132880
 PLACE60138840//PUTATIVE MITOCHONDRIAL CARRIER PROTEIN PET8.//7.40E-59//274aa//47%//P38921
 20 PLACE60140640//Homo sapiens nucleotide binding protein (NBP) mRNA, complete cds.//3.90E-138//262aa//99%//
 AF208536
 PLACE60150510//NUCLEAR PROTEIN SNF7.//1.60E-11//189aa//25%//P39929
 PLACE60154450//PUTATIVE PREOPTIC REGULATORY FACTOR-2 PRECURSOR (PORF-2).//7.30E-36//75aa//
 98%//P18890
 25 PLACE60155910
 PLACE60157310
 PLACE60162100
 PLACE60175640
 PLACE60177880//IGSF5 [Homo sapiens].//3.60E-174//315aa//99%//CAB90447
 30 PLACE60177910
 PLACE60181870
 PLACE60184410//Mus musculus peroxisomal long chain acyl-CoA thioesterase Ib (Pte1b) gene, exon 3 and complete
 cds.//1.00E-43//126aa//69%//AF180801
 PLACE60184870//PHOSPHOLIPID TRANSFER PROTEIN PRECURSOR (LIPID TRANSFER PROTEIN II).//1.50E-
 35 227//330aa//99%//P55058
 PLACE60188630//Mus musculus mRNA for acetylglucosaminyltransferase-like protein.//7.80E-08//317aa//23%//
 AJ006278
 PROST10001100//Zea mays clone AGPZm1 arabinogalactan protein (agp) mRNA, partial cds.//5.80E-05//180aa//
 32%//AF134579
 40 PROST10001360
 PROST10002150
 PROST20007170//Hypothetical Kruppel-Type Zinc Finger Protein(R28830_1)//0//432aa//100%//AAC24608
 PROST20007600//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-.-).//5.90E-29//134aa//44%//Q10348
 PROST20011160
 45 PROST20011800
 PROST20014140
 PROST20014150
 PROST20014650
 PROST20015210//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//3.00E-107//
 50 262aa//85%//P35749
 PROST20015400
 PROST20016760//M-PHASE PHOSPHOPROTEIN 8 (FRAGMENT).//9.00E-157//298aa//99%//Q99549
 PROST20022120
 PROST20024250//ZINC FINGER PROTEIN 136.//1.70E-45//128aa//63%//P52737
 55 PROST20028970//Oryctolagus cuniculus CARP mRNA, complete cds.//4.80E-44//177aa//51%//AF131883
 PROST20033240//EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
 RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2).//8.40E-241//441aa//95%//Q62413
 PROST20035170//Homo sapiens zinc finger protein dp mRNA, complete cds.//3.40E-15//128aa//42%//AF153201

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PROST20035830
 PROST20036280
 PROST20036350//MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYN-
 THETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-
 5 -TRNA LIGASE)].//2.20E-137//651aa//42%//P07814
 PROST20039300//Bos taurus mitochondrial mRNA for xenobiotic/medium-chain fatty acid:CoA ligase form XL-III.//
 1.60E-68//180aa//68%//AJ132751
 PROST20041460
 PROST20042700
 10 PROST20045700//Zea mays clone AGPZm1 arabinogalactan protein (agp) mRNA, partial cds.//5.80E-05//180aa//
 32%//AF134579
 PROST20047440
 PROST20048170
 PROST20050390//CYTOCHROME P450 2J2 (EC 1.14.14.1) (CYPII2) (ARACHIDONIC ACID EPOXYGENASE).//
 15 1.40E-34//188aa//42%//P51589
 PROST20051310//Homo sapiens DEAD-box protein abstrakt (ABS) mRNA, complete cds.//8.50E-134//257aa//99%//
 AF195417
 PROST20052720
 PROST20052850//CYCLIN G-ASSOCIATED KINASE (EC 2.7.1.-).//2.20E-18//107aa//54%//P97874
 20 PROST20054660
 PROST20058860//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEINS B AND B' (SNRNP-B) (SM
 PROTEIN B/B') (SM-B/SM-B').//8.20E-05//134aa//33%//P14678
 PROST20060200
 PROST20062820//TRANSLATION INITIATION FACTOR IF-2.//1.50E-07//102aa//41%//P71613
 25 PROST20063430//BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 2.//8.50E-74//305aa//
 46%//Q12982
 PROST20065100
 PROST20065790//6-PHOSPHOFRUCTOKINASE, TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE 1) (PHOSPHO-
 HEXOKINASE) (PHOSPHOFRUCTO-1-KINASE ISOZYME C) (6-PHOSPHOFRUCTOKINASE, PLATELET TYPE).//
 30 0//697aa//99%//Q01813
 PROST20073280
 PROST20075280//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC
 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.30E-08//245aa//23%//P11799
 PROST20078710
 35 PROST20082430
 PROST20084470//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds.//2.50E-08//
 122aa//28%//AF000413
 PROST20084680
 PROST20084720//CYTOCHROME P450 4F2 (EC 1.14.13.30) (CYP1VF2) (LEUKOTRIENE-B4 OMEGA- HYDROXY-
 40 LASE) (LEUKOTRIENE-B4 20-MONOOXYGENASE) (CYTOCHROME P450- LTB-OMEGA).//1.50E-37//85aa//85%//
 P78329
 PROST20087240
 PROST20093470
 PROST20094000
 45 PROST20097310
 PROST20097360
 PROST20097840//SYNAPSIN I.//1.80E-09//193aa//34%//P17599
 PROST20099090//ADAM 12 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN
 12) (MELTRIN ALPHA).//1.90E-22//73aa//60%//043184 PROST20102190//CALMODULIN.//1.30E-20//98aa//47%//
 50 P02594
 PROST20102500
 PROST20103820
 PROST20105450//SODIUM/HYDROGEN EXCHANGER 6 (NA(+)/H(+) EXCHANGER 6) (NHE-6) (KIAA0267).//
 1.60E-96//214aa//75%//Q92581
 55 PROST20106060
 PROST20108850//MICROSOMAL SIGNAL PEPTIDASE 23 KDA SUBUNIT (EC 3.4.-.-) (SPC22/23).//1.20E-69//
 132aa//100%//PI2280
 PROST20110120

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PROST20114100
 PROST20120070//KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC).//5.00E-05//286aa//
 24%/P33176
 PROST20121570
 5 PROST20122490//Gallus gallus syndesmos mRNA, complete cds.//1.20E-63//139aa//84%/AF095446
 PROST20124000
 PROST20125420
 PROST20127450//Homo sapiens TSC-22 related protein (TSC-22R) mRNA, complete cds.//7.90E-44//95aa//98%/AF153603
 10 PROST20130320
 PROST20138730
 PROST20146590//MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT) (EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN) (TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANUT-REACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN DF3).//3.50E-08//556aa//23%/P15941
 15 PROST20151370//Human probable zinc finger protein H101 mRNA, partial cds.//1.60E-11//104aa//41%/U81557
 PROST20152510//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 100 KDA SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P100 SUBUNIT).//6.00E-17//148aa//34%/I015294
 PROST20152870//Homo sapiens APC2 gene, exon 14.//1.60E-05//195aa//309b/AJ131187
 20 PROST20155370//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//1.10E-72//140aa//55%/Q07231
 PROST20156360
 PROST20159320
 PROST20168600//Homo sapiens six transmembrane epithelial antigen of prostate (STEAP1) mRNA, complete cds.//1.20E-70//237aa//54%/AF186249
 25 PUAEN10000650//Homo sapiens TSC-22 related protein (TSC-22R) mRNA, complete cds.//7.90E-44//95aa//98%/AF153603
 PUAEN10000870
 PUAEN10001640//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.//2.80E-126//270aa//90%/U89345
 30 PUAEN20000800
 PUAEN20001520//L-A VIRUS GAG PROTEIN N-ACETYLTRANSFERASE (EC 2.3.1.-).//1.70E-34//145aa//5196//Q03503
 PUAEN20002470//PR MOV-10.//6.30E-102//405aa//44%/P23249
 35 PUAEN20003120//ENHANCER OF ZESTE HOMOLOG 2 (ENX-1).//0//643aa//97%/Q15910 SALGL10001070//CH-TOG PROTEIN (COLONIC AND HEPATIC TUMOR OVER-EXPRESSED PROTEIN) (KIAA0097).//5.30E-150//297aa//96%/Q14008
 SKMUS20006790
 SKMUS20007260//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: NIAP1 LIGHT CHAIN LC1].//8.10E-05//396aa//23%/P14873
 40 SKMUS20008730//smoothelin large isoform L2 [Homo sapiens].//1.20E-221//217aa//98%/AAF01481
 SKMUS20017400//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE TYPE.//3.20E-97//242aa//81%/P06753
 SKMUS20020770
 SKMUS20026340
 45 SKMUS20040440//60S RIBOSOMAL PROTEIN L3 (HIV-1 TAR RNA BINDING PROTEIN B) (TARBP-B).//3.60E-189//229aa//99%/P39023
 SKMUS20064810
 SKMUS20073150//20-HYDROXYECDYSONE PROTEIN PRECURSOR (20-HE).//1.50E-05//129aa//32%/P29681
 SKMUS20073590//tropomodulin 4 (muscle) [Homo sapiens].//3.90E-58//115aa//100%/NP_037485
 50 SKMUS20079150//splicing factor 3a, subunit 3, 60kD; pre-mRNA splicing factor SF3a (60kD), similar to S. cerevisiae PRP9 (spliceosome-associated protein 61) [Homo sapiens].//9.10E-13//65aa//60%/NP_006793
 SKMUS20091900
 SKNMC10001230//CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (TUMOR SUPPRESSOR CDKN2A).//1.60E-08//105aa//38%/I077617
 55 SKNMC20006350//65 KDA FK506-BINDING PROTEIN PRECURSOR (EC 5.2.1.8) (FKBP65) (FKBPRP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) (IMMUNOPHILIN FKBP65).//1.10E-185//419aa//79%/Q61576
 SKNSH10001010

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- SKNSH20007160
SKNSH20009710//TROPOMYOSIN, CYTOSKELETAL TYPE (TM30-NM)/13.20E-74//174aa//86%//P12324
SKNSH20030640//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)/13.00E-06//127aa//33%//Q62203
- 5 SKNSH20040390
SKNSH20052400//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//3.60E-17//175aa//29%//Q00808
SKNSH20057920//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I)//5.00E-37//197aa//40%//Q14012
SKNSH20068220
- 10 SKNSH20094350
SMINT20000070//Mus musculus mRNA for granuphilin-b, complete cds./2.70E-44//128aa//41%//AB025259
SMINT20002320//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 56 KDA REGULATORY SUBUNIT, BETA ISOFORM (PP2A, B SUBUNIT, B' BETA ISOFORM) (PP2A, B SUBUNIT, B56 BETA ISOFORM) (PP2A, B SUBUNIT, PR61 BETA ISOFORM) (PP2A, B SUBUNIT, R5 BETA ISOFORM)/4.70E-160//299aa//100%//Q15173
- 15 SMINT20006020//faciogenital dysplasia protein 2 [Mus musculus]/4.10E-158//327aa//87%//AF017368
SMINT20006090//Oryctolagus cuniculus mRNA for parchorin, complete cds./7.50E-87//175aa//93%//AB035520
SMINT20007470//TRICHOHYALIN//1.20E-37//492aa//28%//Q07283
SMINT20008110//CALCIUM-TRANSPORTING ATPASE 2C1 (EC 3.6.1.38) (ATP-DEPENDENT CA²⁺ PUMP PMR1)/1.20E-50//165aa//63%//P98194
- 20 SMINT20011830
SMINT20011950//ZINC FINGER PROTEIN 202//1.90E-67//426aa//40%//095125
SMINT20012220
SMINT20013970
SMINT20014610
- 25 SMINT20016150//FERRITIN LIGHT CHAIN (FERRITIN L SLJBUNIT)/3.50E-91//174aa//100%//P02792
SMINT20017310
SMINT20021260
SMINT20023110
SMINT20024140//IG KAPPA CHAIN V-IV REGION B17 PRECURSOR//1.20E-60//134aa//87%//P06314
- 30 SMINT20026200//ENL PROTEIN//1.10E-05//260aa//24%//Q03111
SMINT20028800//tumor supressor protein - fruit fly (Drosophila melanogaster)/2.00E-78//493aa//34%//T13797
SMINT20028840//CMRF35 ANTIGEN PRECURSOR//8.40E-19//136aa//41%//Q08708
SMINT20030740//ZINC FINGER PROTEIN 136//4.50E-194//535aa//63%//P52737
SMINT20031280
- 35 SMINT20035050//GTPASE ACTIVATING PROTEIN BEM2/IPL2//1.20E-07//134aa//26%//P39960
SMINT20035510//Drosophila melanogaster La related protein (larp) mRNA, partial cds./5.40E-39//334aa//30%//AF221108
SMINT20036440//Drosophila melanogaster epsin-like protein mRNA, complete cds./2.90E-69//446aa//41%//AF233291
- 40 SMINT20038660//Homo sapiens HNOEL-iso (HNOEL-iso) mRNA, complete cds./5.60E-201//368aa//99%//AF201945
SMINT20039050//Homo sapiens TRIAD3 mRNA, partial cds./3.20E-86//156aa//100%//AF228527
SMINT20043390
SMINT20044140//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)/3.50E-39//440aa//28%//P51523
SMINT20044730//UBIQUINONE BIOSYNTHESIS PROTEIN AARF//6.20E-22//272aa//27%//P27854
- 45 SMINT20045470
SMINT20045830
SMINT20045890
SMINT20047290
SMINT20048720
- 50 SMINT20049920//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5)/4.10E-39//132aa//57%//P49902
SMINT20052130//Rattus norvegicus mRNA for gankyrin homologue, complete cds./9.20E-07//104aa//33%//AB022014
SMINT20054050//ABC1 PROTEIN HOMOLOG PRECURSOR//1.40E-98//467aa//45%//Q92338
SMINT20056230//Ig mu chain precursor, membrane-bound (clone 201) -human/5.60E-233//422aa//78%//S14683
- 55 SMINT20056240
SMINT20062050//PLECTIN//7.50E-17//436aa//25%//P30427
SMINT20067080
SMINT20070620

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SMINT20074330//tektin A1 [Strongylocentrotus purpuratus]//3.10E-26//125aa//45%//M97188
SMINT20077920
SMINT20077960//GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN)
(AGEL).//3.30E-246//459aa//99%//P06396
5 SMINT20081330
SMINT20083290//IG ALPHA-1 CHAIN C REGION.//4.40E-196//352aa//99%//P01876
SMINT20084910
SMINT20085310
SMINT20085450
10 SMINT20086250//GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR.//2.20E-40//70aa//97%//P23434
SMINT20086720//ZINC FINGER PROTEIN 191.//1.40E-29//109aa//55%//014754
SMINT20088440//IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.//5.10E-44//117aa//78%//P06310
SMINT20088690
SMINT20089210
15 SMINT20089600//Homo sapiens mRNA for PICK1, complete cds.//13.10E-145//278aa//100%//AB026491
SMINT20091190//IG ALPHA-1 CHAIN C REGION.//3.70E-198//353aa//99%//P01876
SMINT20092120
SMINT20092160
SMINT20093630
20 SMINT20094150
SMINT20094680//Homo sapiens mawbp mRNA for MAWD binding protein, complete cds.//2.80E-50//77aa//100%//
AB049758
SPLEN20005160
SPLEN20005370
25 SPLEN20006950
SPLEN20011350
SPLEN20012450
SPLEN20015030
SPLEN20015100//HYPOTHETICAL 72.5 KDA PROTEIN C2F7.10 IN CHROMOSOME I.//7.50E-16//121aa//36%//
30 Q09701
SPLEN20016500
SPLEN20017610
SPLEN20017810
SPLEN20019120
35 SPLEN20020530
SPLEN20023430
SPLEN20023540//H.sapiens mRNA for F25B3.3 kinase like protein from C. elegans.//1.50E-205//385aa//99%//
Y12336
SPLEN20023850//DNA REPAIR PROTEIN RAD18.//3.00E-56//469aa//30%//P53692
40 SPLEN20024190//EGF-containing fibulin-like extracellular matrix protein 1; fibrillin-like [Homo sapiens]//3.70E-192//
327aa//99%//NP_061489
SPLEN20024510
SPLEN20024620//Homo sapiens mRNA for acetyl LDL receptor, complete cds.//1.00E-217//401aa//100%//D86864
SPLEN20024770//Rattus norvegicus (rsec6) mRNA, complete cds.//2.10E-88//545aa//31%//U32575
45 SPLEN20024930//Rattus norvegicus PIPP mRNA for proline-rich inositol polyphosphate 5-phosphatase, complete
cds.//0//639aa//91%//AB032551
SPLEN20029170
SPLEN20036780
SPLEN20039180//TENSIN.//2.70E-135//341aa//653o//Q04205
50 SPLEN20040780//C B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1
B).//5.10E-12//110aa//37%//Q62267
SPLEN20041810//BC-2 protein [Homo sapiens]//4.00E-24//59aa//96%//AF042384
SPLEN20042200//TRANSCRIPTIONAL REPRESSOR CTCF.//8.40E-22//127aa//33%//P49711
SPLEN20043430
55 SPLEN20043460
SPLEN20043680//DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM
GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).//7.30E-171//325aa//99%//
P18074

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SPLEN20045550
 SPLEN20048800//Homo sapiens mRNA for N-Acetylglucosamine kinase.//1.90E-51//104aa//100%//AJ242910
 SPLEN20049840//M.musculus mRNA for myosin I.//0//1093aa//89%//X97650
 SPLEN20050090//TRICHOHYALIN.//7.20E-17//554aa//23%//P37709
 5 SPLEN20051420
 SPLEN20054160//Dof protein [Drosophila melanogaster]//9.60E-14//222aa//29%//AJ010641
 SPLEN20054500//Homo sapiens mRNA for putative dipeptidase.//7.10E-130//244aa//100%//AJ295149
 SPLEN20055600//ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP).//3.00E-56//155aa//63%//P24278
 SPLEN20057830//REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1).//1.10E-16//139aa//43%//P49646
 10 SPLEN20057900//Homo sapiens N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase mRNA, complete cds.//9.00E-75//130aa//93%//AF187072
 SPLEN20058180
 SPLEN20059270//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//7.20E-61//497aa//31%//P14373
 SPLEN20062830
 15 SPLEN20063250//zinc finger protein nocA - fruit fly (Drosophila melanogaster)//9.00E-16//364aa//30%//A55929
 SPLEN20063890//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KDA PROTEIN).//2.60E-118//242aa//94%//Q06828
 SPLEN20067010
 SPLEN20071820//Homo sapiens DNA polymerase mu (Pol mu) mRNA, complete cds.//4.70E-62//116aa//100%//AF176097
 20 SPLEN20073500//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 2 (B94 PROTEIN).//3.50E-10//463aa//25%//Q03169
 SPLEN20073880
 SPLEN20076190
 25 SPLEN20076470//KINESIN LIGHT CHAIN (KLC).//2.40E-18//137aa//38%//P46825
 SPLEN20080070//TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (EC 3.2.1.51) (ALPHA-L-FUCOSIDA I) (ALPHA-L-FUCOSIDE FUCOHYDROLASE).//4.70E-253//359aa//98%//P04066
 SPLEN20081640
 SPLEN20085910//Homo sapiens protein activator of the interferon-induced protein kinase (PACT) mRNA, complete cds.//2.90E-23//52aa//100%//AF072860
 30 SPLEN20087370
 SPLEN20087860
 SPLEN20090880//HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN PRECURSOR (AW-24).//1.40E-66//153aa//83%//P05534
 35 SPLEN20098030//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//4.00E-18//267aa//26%//Q13263
 SPLEN20100040//258.1 1 KDA PROTEIN C210RF5 (KIAA0933).//7.90E-46//223aa//43%//Q9Y3R5
 SPLEN20101950//SODIUM/HYDROGEN EXCHANGER 6 (NA(+)/H(+) EXCHANGER 6) (NHE-6) (KIAA0267).//7.70E-12//353aa//61%//Q92581
 40 SPLEN20104150
 SPLEN20104690
 SPLEN20105100
 SPLEN20108000//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//9.30E-73//155aa//94%//AF078850
 45 SPLEN20108460
 SPLEN20110180//Homo sapiens golgi membrane protein GP73 mRNA, complete cds.//1.60E-162//347aa//91%//AF236056
 SPLEN20110210
 SPLEN20110860
 50 SPLEN20111450
 SPLEN20114190
 SPLEN20116720//Homo sapiens misato mRNA, partial cds.//1.00E-277//481aa//89%//AF272833
 SPLEN20117580
 SPLEN20118050//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//1.00E-123//240aa//9796//P21810
 55 SPLEN20121790
 SPLEN20125230
 SPLEN20126110

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SPLEN20135030//Homo sapiens PDZ-LIM protein mystique mRNA, complete cds.//3.30E-92//178aa//97%//AY007729
 SPLEN20136700
 SPLEN20136730//Homo sapiens RAB-like protein 2A (RABL2A) mRNA, complete cds.//9.30E-41//102aa//90%//
 AF095350
 5 SPLEN20137530
 SPLEN20138600//NUMB protein [Homo sapiens].//1.00E-97//102aa//100%//AAD01548
 SPLEN20139100//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementarity-
 determining regions mRNA, complete cds.//2.30E-227//490aa//85%//M87789
 SPLEN20139360//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//5.10E-35//
 10 295aa//32%//P07199
 SPLEN20175920
 SPLEN20176130//Homo sapiens mRNA for ALEX1, complete cds.//9.90E-21//161aa//132%//AB039670
 SPLEN20177400
 SPLEN20180980//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE) (METRS).//
 15 3.40E-57//133aa//87%//P56192
 SPLEN20181570//TRICHOHYALIN.//7.80E-45//832aa//23%//P37709
 SPLEN20182850
 SPLEN20182990//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//1.90E-49//586aa//26%//
 U65079
 20 SPLEN20183020//BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
 PRECURSOR (HSPG) (PERLECAN) (PLC).//1.20E-24//128aa//46%//Q05793
 SPLEN20183950
 SPLEN20187490//RESTIN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CLIP-170) (REED- STERNBERG IN-
 25 INTERMEDIATE FILAMENT ASSOCIATED PROTEIN).//5.10E-09//411aa//22%//P30622
 SPLEN20190080
 SPLEN20190430//NEURALIZED PROTEIN.//2.80E-09//181aa//27%//P29503
 SPLEN20190770
 SPLEN20191020//Homo sapiens MIST mRNA, partial cds.//1.50E-207//376aa//99%//AB032369
 SPLEN20192570
 30 SPLEN20193230
 SPLEN20193490
 SPLEN20193750
 SPLEN20193790//INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXA
 (INTERFERON- INDUCED PROTEIN P78) (IFI-78K).//0//572aa//98%//P20591
 35 SPLEN20195710//KINESIN LIGHT CHAIN (KLC).//5.80E-28//145aa//45%//P46824
 SPLEN20197090
 SPLEN20197740
 SPLEN20197930//Rattus norvegicus putative transcription factor LUZP (Luzp) mRNA, complete cds.//6.10E-124//
 275aa//90%//AF181259
 40 SPLEN20198390//TIPD PROTEIN.//2.80E-52//307aa//37%//O15736
 SPLEN20199850
 SPLEN20200070
 SPLEN20200340
 SPLEN20201830//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//2.50E-152//283aa//
 45 100%//P21810
 SPLEN20203590
 SPLEN20204670
 SPLEN20205120
 TESOP10000350
 50 TESOP10001600
 TESTI10000190//MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT) (EPISIALIN) (TU-
 MOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN) (TUMOR-ASSOCIATED EPITHELIAL MEM-
 BRANE ANTIGEN) (EMA) (H23AG) (PEANUT- REACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSO-
 CIATED ANTIGEN DF3).//1.40E-23//667aa//28%//P15941
 55 TESTI10000850
 TESTI10001570//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.30E-148//598aa//4696//P51523
 TESTI20004310//TRICHOHYALIN.//1.40E-07//247aa//25%//P22793
 TESTI20005980

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TESTI20006160//CALCIUM-BINDING PROTEIN.//1.10E-11//260aa//28%/P35085
 TESTI20006830//GAR2 PROTEIN.//2.90E-05//221aa//19%/P41891
 TESTI20012080//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.20E-22//217aa//35%/P38584
 TESTI20012360
 5 TESTI20016970
 TESTI20019590
 TESTI20028020
 TESTI20029100//FIBROSIN (FRAGMENT).//1.60E-10//70aa//48%/Q60791
 TESTI20030200//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMI-
 10 NASE) (RNA EDITING ENZYME 1).//1.90E-30//192aa//38%/P51400
 TESTI20030440//TRICHOHYALIN.//2.80E-21//412aa//26%/P37709
 TESTI20030610
 TESTI20031310//ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR (ACT).//7.80E-22//423aa//99%/P01011
 TESTI20031410//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//6.10E-11//449aa//24%/Q03410
 15 TESTI20032770//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//1.40E-07//121aa//37%/P40602
 TESTI20034750
 TESTI20035330
 TESTI20035790//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//
 20 2.30E-44//346aa//37%/Q08170
 TESTI20038240//Mus musculus neprilysin-like metallopeptidase 1 (N11) mRNA, complete cds.//0//770aa//77%/AF176569
 TESTI20040850
 TESTI20041630//Mus musculus mRNA for type II cytokeratin, complete cds.//1.30E-151//407aa//75%/AB033744
 25 TESTI20043130
 TESTI20043180//mouse mRNA for megakaryocyte potentiating factor, complete cds.//8.40E-06//392aa//24%/D86370
 TESTI20043220//ORM1 PROTEIN.//6.40E-21//138aa//37%/P53224
 TESTI20043910
 TESTI20043990//APOMUCIN (MUCIN CORE PROTEIN) (FRAGMENT).//8.70E-64//283aa//53%/P12021
 30 TESTI20044900//Strongylocentrotus purpuratus radial spokehead mRNA, complete cds.//2.50E-150//447aa//61%/U73123
 TESTI20045390//Homo sapiens adican mRNA, complete cds.//1.80E-173//632aa//47%/AF245505
 TESTI20045740
 TESTI20046110
 35 TESTI20046490//Homo sapiens B2 gene partial cDNA, clone B2E.//4.30E-33//284aa//34%/AJ002220
 TESTI20046540
 TESTI20046870//RETINAL-BINDING PROTEIN (RALBP).//4.00E-06//244aa//23%/P49193
 TESTI20046890//Mus musculus axotrophin mRNA, complete cds.//2.30E-40//173aa//53%/AF155739
 TESTI20047370//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.90E-22//695aa//
 40 28%/P54258
 TESTI20047930//Homo sapiens NY-REN-2 antigen mRNA, complete cds.//1.50E-191//530aa//67%/AF155095
 TESTI20049060//H.sapiens mRNA for SIRP-beta1.//2.50E-31//172aa//46%/Y10376
 TESTI20049410
 TESTI20049990
 45 TESTI20050170
 TESTI20050400
 TESTI20050720//SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (EC 2.8.3.5) (SUC-
 CINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT).//1.40E-208//519aa//74%/P55809
 TESTI20051200//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP
 50 ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL-
 TRANSFERASE) (GALNAC-T1).//6.10E-50//189aa//49%/Q10472
 TESTI20051730//MALTOSE PERMEASE.//2.20E-05//327aa//23%/Q45632
 TESTI20052670
 TESTI20053070//HYPOTHETICAL WD-REPEAT PROTEIN SLL0163.//5.00E-06//172aa//28%/Q55563
 55 TESTI20053260
 TESTI20053780
 TESTI20053800
 TESTI20053950

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TESTI20054700//Streptococcus pneumoniae strain g375 surface protein PspC (pspC) gene, pspC-8. 1 allele, complete cds.//6.70E-11//219aa//32%//AF154015

TESTI20055680//TRANSLATION INITIATION FACTOR IF-2.//5.90E-08//98aa//41%//060841

TESTI20055880

5 TESTI20056030//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.//3.60E-103//316aa//6896//AF204231

TESTI20057200

TESTI20057430//ZINC FINGER PROTEIN 8 (ZINC FINGER PROTEIN HF.18) (FRAGMENT).//3.00E-307//543aa//99%//P17098

10 TESTI20057590//TYROSINE-PROTEIN KINASE-LIKE 7 PRECURSOR (COLON CARCINOMA KINASE-4) (CCK-4).//7.80E-07//152aa//27%//Q13308

TESTI20057840//INHIBITOR OF APOPTOSIS PROTEIN (IAP) (INHIBITOR OF T CELL APOPTOSIS PROTEIN).//7.20E-08//86aa//36%//Q90660

TESTI20057880//CALDESMON (CDM).//6.20E-08//203aa//29%//P12957

15 TESTI20058350//SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 55 KDA REGULATORY SUBUNIT B, GAMMA ISOFORM (PP2A, SUBUNIT B, B-GAMMA ISOFORM) (PP2A, SUBUNIT B, B55-GAMMA ISOFORM) (PP2A, SUBUNIT B, PR55-GAMMA ISOFORM) (PP2A, SUBUNIT B, R2-GAMMA ISOFORM).//2.00E-232//426aa//99%//P50410

TESTI20058920//TUBULIN ALPHA-3/ALPHA-7 CHAIN.//3.50E-148//277aa//98%//P05214

20 TESTI20059080//Homo sapiens hyaluronidase (LUCA-3) mRNA, complete cds.//2.40E-170//298aa//100%//AF040710

TESTI20059330

TESTI20059370

TESTI20059480

TESTI20059790

25 TESTI20059810//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.50E-153//536aa//52%//P51523

TESTI20060080//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.30E-09//236aa//24%//P39922

TESTI20060150

TESTI20060350

TESTI20060450

30 TESTI20060830//Mus musculus mRNA for MIWI (piwi), complete cds.//0//824aa//94%//AB032604

TESTI20061090

TESTI20061200//NITRITE EXTRUSION PROTEIN (NITRITE FACILITATOR).//4.90E-05//379aa//23%//P46907

TESTI20062120//poly(A)-specific ribonuclease (deadenylation nuclease) ; deadenylation nuclease [Homo sapiens]//1.00E-38//144aa//36%//NP_002573

35 TESTI20062180

TESTI20062580

TESTI20063330

TESTI20063410

TESTI20063600

40 TESTI20064370

TESTI20064530//microtubule-associated protein like echinoderm EMAP [Homo sapiens].//1.00E-173//562aa//48%//XP_009139

TESTI20064650//Rattus norvegicus myr 6 myosin heavy. chain mRNA, complete cds.//0//645aa//91%//U60416

TESTI20064990

45 TESTI20065650//INNER CENTROMERE PROTEIN (INCENP).//1.00E-14//273aa//27%//P53352

TESTI20066150

TESTI20066170

TESTI20066280

TESTI20066330//FIBRONECTIN PRECURSOR.//9.10E-12//408aa//22%//Q91740

50 TESTI20066590

TESTI20066650//CELL DIVISION CONTROL PROTEIN 25.//2.20E-18//216aa//32%//P04821

TESTI20067350

TESTI20067440//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//2.90E-11//553aa//20%//P25386

TESTI20067480//ZINC FINGER PROTEIN 184 (FRAGMENT).//8.60E-134//421aa//50%//Q99676

55 TESTI20068530

TESTI20068790//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2. 9/ER2.6).//7.50E-06//240aa//28%//P29128

TESTI20068940

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TESTI20070400//Homo sapiens CTL2 gene.//5.90E-229//694aa//55%//AJ245621
 TESTI20070740
 TESTI20071130//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM.//6.30E-09//399aa//23%//Q02566
 TESTI20071630//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.10E-44//203aa//42%//
 5 P48060
 TESTI20073460
 TESTI200752401//HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961.//3.20E-145//492aa//56%//Q9Y2G7
 TESTI20076570//Homo sapiens mitogen-activated protein kinase phosphatase x (MKPX) mRNA, complete cds.//
 7.20E-66//126aa//100%//AF165519
 10 TESTI20076920
 TESTI20079060
 TESTI20079220//ZINC FINGER PROTEIN 29 (ZFP-29).//2.00E-73//281aa//49%//Q07230
 TESTI20079980//SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-1 (DISHEVELLED-1) (DSH HO-
 MOLOG 1).//7.10E-212//413aa//93%//P51141
 15 TESTI20080460
 TESTI20081890//SPA-1 like protein p1294 [Rattus norvegicus]//5.80E-129//385aa//41%//AF026504
 TESTI20083890
 TESTI20084250//OXYSTEROL-BINDING PROTEIN.//3.70E-183//561aa//62%//P16258
 TESTI20085670
 20 TESTI20086840//CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//3.40E-09//181aa//29%//P05099
 TESTI20088840//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//2.60E-73//258aa//31%//Q62158
 TESTI20089290
 TESTI20090180
 TESTI20090970
 25 TESTI20091360
 TESTI20092170
 TESTI20093900
 TESTI20094620
 TESTI20095200//HYPOTHETICAL 98.3 KDA PROTEIN B0495.7 IN CHROMOSOME II.//1.30E-63//328aa//40%//
 30 Q09216
 TESTI20095440//probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)//1.00E-25//98aa//55%//
 S67133
 TESTI20095770//NEDD1 PROTEIN (FRAGMENT).//5.80E-297//648aa//85%//P33215
 TESTI20095880//HYPOTHETICAL SYMPORTER SLL1374.//3.80E-26//243aa//27%//P74168
 35 TESTI20097270
 TESTI20099350//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B)
 (NMMHC-B).//1.50E-26//566aa//23%//P35580
 TESTI20100090//Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds.//5.00E-161//317aa//
 93%//AF134838
 40 TESTI20102390
 TESTI20103690//Columba livia mRNA for 5'-nucleotidase.//2.70E-114//324aa//66%//AJ131243
 TESTI20104090//TRANSCRIPTIONAL ENHANCER FACTOR TEF-4 (EMBRYONIC TEA DOMAIN-CONTAINING
 FACTOR) (ETF) (ETEF-1) (TEAD-2).//1.60E-228//450aa//92%//P48301
 TESTI20105130//MYOTUBULARIN.//4.30E-95//537aa//38%//Q13496
 45 TESTI20105910//AMILORIDE-SENSITIVE SODIUM CHANNEL DELTA-SUBUNIT (EPITHELIAL NA+ CHANNEL
 DELTA SUBUNIT) (DELTA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 DELTA SUBUNIT) (SCNED) (DEL-
 TA NACH).//0//636aa//97%//P51172
 TESTI20106170//Mus musculus spermatid WD-repeat protein mRNA, complete cds.//2.20E-167//367aa//83%//
 AF274321
 50 TESTI20106820//PROTEIN KINASE C, ETA TYPE (EC 2.7.1.-) (NPKC-ETA) (PKC-L).//5.40E-53//97aa//100%//
 P24723
 TESTI20107240//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EUKARYOTIC
 TRANSLATION INITIATION FACTOR 3 LARGE SUBUNIT) (PNLA-35).//5.60E-07//428aa//22%//Q40554
 TESTI20107320//G1/S-SPECIFIC CYCLIN C-TYPE.//1.20E-05//130aa//26%//P93411
 55 TESTI20107340
 TESTI20108060//SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16)
 (PP-1B).//1.10E-78//145aa//100%//P37140
 TESTI20112540//CALDESMON (CDM).//9.10E-06//203aa//30%//P12957

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TESTI20112860//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//1.60E-54//290aa//40%/P25323
 TESTI20113150
 TESTI20113940
 TESTI20114480//Human 1(3)mbt protein homolog mRNA, complete cds.//7.10E-146//582aa//49%/U89358
 5 TESTI20116050
 TESTI20116120//Aegilops squarrosa partial GAG56D gene for gamma-gliadin, accession Clae 24.//3.10E-07//93aa//40%/AJ389681
 TESTI20117500
 TESTI20118460
 10 TESTI20120500
 TESTI20120900
 TESTI20121040//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//8.60E-13//91aa//39%/P49596
 TESTI20121710//HYPOTHETICAL 57.5 KDA PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//5.00E-08//292aa//26%/P53214
 15 TESTI20122070//Xenopus laevis ER1 mRNA, complete cds.//1.80E-78//341aa//49%/AF015454
 TESTI20122440
 TESTI20124440
 TESTI20125280//M-PROTEIN, STRIATED MUSCLE.//3.60E-68//295aa//46%/Q02173
 20 TESTI20125440
 TESTI20125920//G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN).//5.20E-199//367aa//98%/Q13098
 TESTI20126280//Mus musculus STAP mRNA for sperm tail associated protein, complete cds.//4.60E-213//769aa//57%/AB029919
 25 TESTI20130530//INSULIN-DEGRADING ENZYME (EC 3.4.24.56) (INSULYSIN) (INSULINASE) (INSULIN PROTEASE).//1.60E-237//464aa//94%/P14735
 TESTI20131440//CARBOXYPEPTIDASE A1 PRECURSOR (EC 3.4.17.1).//2.80E-107//332aa//58%/P15085
 TESTI20132310
 TESTI20132680
 30 TESTI20134010
 TESTI20134270
 TESTI20134680//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.40E-08//796aa//19%/Q02224
 TESTI20134970//M.musculus Tenr mRNA for RNA binding protein.//5.50E-265//559aa//88%/X84693
 TESTI20136010//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//1.10E-11//438aa//23%/P14105
 35 TESTI20140970//V_segment translation product [Homo sapiens].//6.30E-51//101aa//99%/AAC80210
 TESTI20142480
 TESTI20142540//IMPV17 PROTEIN.//8.00E-62//116aa//98%/P39210
 TESTI20143180//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.30E-09//507aa//22%/Q02224
 40 TESTI20144390//TESTIS-SPECIFIC PROTEIN PBS13.//6.40E-76//251aa//63%/Q01755
 TESTI20145780//Mus musculus mRNA for SH2-containing leukocyte protein 65.//1.20E-13//91aa//36%/Y17159
 TESTI20148380//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//2.50E-05//193aa//2296/P31948
 TESTI20149880
 TESTI20150420//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//4.50E-09//129aa//34%/Q07960
 45 TESTI20150920//PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22.//2.60E-16//193aa//34%/P22194
 TESTI20151050
 50 TESTI20151800
 TESTI20152490
 TESTI20153310//LAMIN B3.//6.30E-13//104aa//41%/P48680
 TESTI20154370//HYALURONAN MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY).//1.10E-07//300aa//21%/075330
 55 TESTI20159380
 TESTI20161010
 TESTI20162780//COTE1 PROTEIN.//1.00E-107//207aa//99%/P81408
 TESTI20162980//DNA-DAMAGE INDUCIBLE PROTEIN DDI1.//1.80E-39//174aa//48%/P40087

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TESTI20164210//PROTEIN KINASE C-BINDING PROTEIN NELL1 (NEL-LIKE PROTEIN 1) (FRAGMENT).//1.60E-88//163aa//92%//Q92832
 TESTI20165680
 TESTI20165990
 5 TESTI20166290//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//3.00E-223//426aa//93%//AF155112
 TESTI20166670//HOMEBOX PROTEIN HOX-B1 (HOX-2I).//6.70E-06//224aa//29%//P14653
 TESTI20167580
 TESTI20168880//BREAKPOINT CLUSTER REGION PROTEIN (EC 2.7.1.-).//2.10E-23//57aa//92%//P11274
 TESTI20169500//HYPOTHETICAL 51.9 KDA PROTEIN C27F1.04C IN CHROMOSOME I.//9.50E-17//428aa//25%//
 10 Q10173
 TESTI20170170//Homo sapiens mRNA for chondroitin-4-sulfotransferase (C4ST gene).//1.10E-53//277aa//40%//
 AJ269537
 TESTI20170280
 TESTI20170690
 15 TESTI20170890
 TESTI20171070//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-4 (DNA-BINDING PROTEIN
 TAXREB67) (CYCLIC AMP RESPONSE ELEMENT-BINDING PROTEIN 2) (CREB2).//2.60E-63//136aa//91%//
 P18848
 TESTI20173050
 20 TESTI20173110
 TESTI20173960//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.90E-104//335aa//48%//
 Q05481
 TESTI20175370//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//1.00E-
 11//290aa//25%//P14105
 25 TESTI20176450//thioredoxin interacting factor [Mus musculus].//1.00E-75//300aa//46%//AAG32665
 TESTI20179230
 TESTI20179510
 TESTI20180600//Homo sapiens HOM-TES-85 tumor antigen mRNA, complete cds.//8.10E-106//202aa//99%//
 AF124430
 30 TESTI20182210
 TESTI20182760//AMILORIDE-SENSITIVE SODIUM CHANNEL DELTA-SUBUNIT (EPITHELIAL NA+ CHANNEL
 DELTA SUBUNIT) (DELTA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 DELTA SUBUNIT) (SCNED) (DEL-
 TA NACH).//5.90E-185//336aa//99%//P51172
 TESTI20183680//EARLY NODULIN 20 PRECURSOR (N-20).//5.10E-08//127aa//37%//P93329
 35 TESTI20184280
 TESTI201847501//LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).//2.30E-200//377aa//99%//P25391
 TESTI20184760//ZINC FINGER PROTEIN 29 (ZFP-29).//9.70E-74//281aa//49%//Q07230
 TESTI20184820
 TESTI20186110
 40 TESTI20192570
 TESTI20193080//GAR22 PROTEIN.//5.10E-153//313aa//92%//Q99501
 TESTI20193520
 TESTI20194880//PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER).//1.50E-
 11//288aa//30%//O15534
 45 TESTI20196690//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete
 cds.//9.10E-114//224aa//92%//AF026954
 TESTI20196970//THIMET OLIGOPEPTIDASE (EC 3.4.24.15) (ENDOPEPTIDASE 24.15) (MP78).//4.00E-106//
 147aa//100%//P52888
 TESTI20197030
 50 TESTI20197290
 TESTI20197600//TRANSCRIPTIONAL REPRESSOR CTCF.//5.30E-120//271aa//82%//P49711
 TESTI20198540
 TESTI20198600
 TESTI20199110//disintegrin-like testicular metalloproteinase (EC 3.4.24.-) IVb - crab-eating macaque (fragment) //
 55 1.00E-167//331aa//84%//I65253
 TESTI20199980
 TESTI20200120
 TESTI20200840

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TESTI20201760//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.70E-09//189aa//25%//Q15431
 TESTI20202830
 TESTI20204260
 TESTI20205100//TRICHOHYALIN.//2.60E-15//343aa//24%//P37709
 5 TESTI20205150
 TESTI20205250//phosphatidylinositol-4-phosphate 5-kinase homolog T3K9.2 - *Arabidopsis thaliana* //4.20E-21//194aa//33%//T02098
 TESTI20207170//Human testis-specific protein (TSPY) mRNA, complete cds.//6.80E-111//231aa//96%//U58096
 TESTI20209050//HYPOTHETICAL 113.1 KDA PROTEIN IN PRES-FET4 INTERGENIC REGION.//1.90E-05//462aa//22%//Q04893
 10 TESTI20210030
 TESTI20210570//RETINAL-BINDING PROTEIN (RALBP).//5.00E-53//327aa//36%//P49193
 TESTI20211380
 TESTI20212970//PUTATIVE ATP-DEPENDENT RNA HELICASE YIR002C.//5.90E-85//458aa//32%//P40562
 15 TESTI20214630
 TESTI20215310//Homo sapiens calcyclin binding protein mRNA, complete cds.//6.60E-95//182aa//100%//AF057356
 TESTI20219110//TYROSINE-PROTEIN KINASE-LIKE 7 PRECURSOR (COLON CARCINOMA KINASE-4) (CCK-4).//4.00E-23//53aa//100%//Q13308
 TESTI20219390
 20 TESTI20220230//Bos taurus Reissner's fiber glycoprotein I mRNA, partial cds.//1.20E-10//77aa//50%//AF078930
 TESTI20221790
 TESTI20222030//Homo sapiens very long-chain acyl-CoA synthetase (BG1) mRNA, complete cds.//6.10E-172//643aa//50%//AF179481
 TESTI20222460//DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM.//1.50E-138//589aa//46%//Q39575
 25 TESTI20223380
 TESTI20226520//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//6.70E-06//164aa//30%//P38160
 TESTI20227380//DEAD BOX PROTEIN 4 (VASA HOMOLOG) (RVLG).//1.10E-263//577aa//86%//Q64060
 TESTI20228120//RHO-GTPASE-ACTIVATING PROTEIN 6 (RHO-TYPE GTPASE-ACTIVATING PROTEIN RHOG-APX-1) (FRAGMENT).//4.50E-12//164aa//34%//O54834
 30 TESTI20228740//ZINC FINGER PROTEIN 135.//3.50E-25//132aa//43%//P52742
 TESTI20244220//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//6.50E-11//77aa//42%//P19706
 TESTI20244430//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//3.70E-15//173aa//35%//P16157
 TESTI20244460//ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).//3.60E-34//209aa//37%//F43188
 35 TESTI20244730//Mus musculus alpha/beta hydrolase-1 mRNA, complete cds.//8.20E-113//266aa//81%//AF189764
 TESTI20245600//HYPOTHETICAL 118.4 KDA PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//4.50E-05//236aa//27%//P47179
 TESTI20245860
 40 TESTI20246410
 TESTI20246480//Homo sapiens germline specific RNA binding protein (DAZL1) mRNA, complete cds.//5.00E-22//86aa//55%//U66726
 TESTI20247440//Human BLu protein testis isoform (BLu) mRNA, complete cds.//5.40E-45//91aa//96%//U70880
 TESTI20248850
 45 TESTI20249360//Homo sapiens DEME-6 mRNA, partial cds.//4.70E-94//299aa//56%//AF007170
 TESTI20250220//TRICHOHYALIN.//5.40E-54//537aa//30%//P37709
 TESTI20250630//Columba livia mRNA for 5'-nucleotidase.//3.80E-115//328aa//66%//AJ131243
 TESTI20251440//Rattus norvegicus (rsec6) mRNA, complete cds.//3.80E-31//379aa//2896//U32575
 TESTI20251610//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.10E-07//182aa//26%//O02668
 50 TESTI20251740//FYN-BINDING PROTEIN (SLP-76 ASSOCIATED PROTEIN) (SLAP-130).//6.30E-16//88aa//50%//O15117
 TESTI20252690//SEGMENT POLARITY PROTEIN DISHEVELLED.HOMOLOG DVL-3 (DISHEVELLED-3) (DSH HOMOLOG 3) (KIAA0208).//4.60E-137//304aa//85%//Q92997
 55 TESTI20254030//Homo sapiens actin-binding double-zinc-finger protein (abLIM) mRNA, complete cds.//6.70E-150//280aa//96%//AF005654
 TESTI20254090
 TESTI20254480

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TESTI20254990//ZINC FINGER PROTEIN GLI3 (NEURAL SPECIFIC DNA BINDING PROTEIN XGLI3) (XGLI-3)//
6.50E-46//105aa//75%//Q91660

TESTI20255460//Mus musculus mRNA for MIWI (piwi), complete cds.//1.50E-225//864aa//49%//AB032604

TESTI20256560//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//5.70E-05//590aa//19%//
5 P32380

TESTI20257910//HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN G - PRECURSOR (HLA G ANTI-
GEN)//1.90E-122//223aa//100%//P17693

TESTI20258720//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2)//1.20E-10//
233aa//27%//P16157

10 TESTI20259110

TESTI20259200

TESTI20260140

TESTI20260640//helicase II homolog - fruit fly (Drosophila sp.)//2.70E-27//374aa//27%//T13889

TESTI20261040//DPY-19 PROTEIN.//2.10E-47//316aa//34%//P34413

15 TESTI20261160//Mus musculus rasGAP-activating-like protein mRNA, complete cds.//1.60E-21//129aa//41%//
AF086714

TESTI20261680//HEAT SHOCK PROTEIN 30C.//1.70E-08//136aa//27%//P30218

TESTI20262150//Rattus norvegicus mRNA for voltage-gated ca channel, complete cds.//0//822aa//87%//AB018253

TESTI20262940//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL)//5.70E-10//218aa//25%//P38160

20 TESTI20264530//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-//5.60E-18//219aa//34%//
P49695

TESTI20264910

TESTI20265150

TESTI20265340

25 TESTI20265890

TESTI20266050//52 KDA RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//2.10E-
77//472aa//38%//P19474

TESTI20268240//Homo sapiens membrane-associated nucleic acid binding protein mRNA, partial cds.//1.90E-52//
412aa//36%//AF255303

30 TESTI20269250

TESTI20269360

TESTI20270130//FIBRILLARIN.//2.10E-11//97aa//43%//Q22053

TESTI20271790//Human p76 mRNA, complete cds.//6.9e-317//496aa//99%//U81006

TESTI20272380

35 TESTI20274960//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//7.90E-126//342aa//63%//P51522

TESTI20277300

TESTI20278280//Mus musculus p53 apoptosis-associated target (Perp) mRNA, complete cds.//3.40E-84//155aa//
88%//AF249870

TESTI20282420//Mus musculus EPCS26 mRNA, complete cds.//2.40E-19//122aa//3396//AF250838

40 TESTI20282530//ZINC FINGER PROTEIN 135.//1.60E-56//271aa//39%//P52742

TESTI20282900

TESTI20284260//HISTONE H2B F (H2B 291A)//2.10E-22//120aa//43%//P10853

TESTI20285230//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMI-
NASE)(RNA EDITING ENZYME 1)//2.10E-20//192aa//38%//P51400

45 TESTI20286590//Human type 3 inositol 1,4,5-trisphosphate receptor (ITPR3) mRNA, complete cds.//1.00E-93//
185aa//100%//U01062

TESTI20287760

THYMU10004280//ZINC-FINGER PROTEIN HT2A (72 KDA TAT-INTERACTING PROTEIN)//7.90E-13//87aa//42%//
Q13049

50 THYMU20006020//ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR
(EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH)//2.60E-120//229aa//99%//P50213

THYMU20007020

THYMU20007750

THYMU20008000

55 THYMU20009460

THYMU20009500

THYMU20009710

THYMU20010180//MOB1 PROTEIN (MPS1 BINDER 1)//2.60E-31//136aa//50%//P40484

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THYMU20010710
 THYMU20012020
 THYMU20012560
 THYMU20013250//LIM DOMAIN KINASE 2 (EC 2.7.1.-) (LIMK-2)//3.50E-213//354aa//99%//P53671
 5 THYMU20013810//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//2.30E-88//138aa//96%//U63127
 THYMU20014430
 THYMU20017270
 THYMU20018250
 THYMU20018390
 10 THYMU20019000
 THYMU20019260//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1)//6.80E-49//137aa//68%//Q03923
 THYMU20020370
 THYMU20020800//LMBR1 long form [Mus musculus]//3.00E-69//198aa//55%//AAF91092
 15 THYMU20021090//Homo sapiens Sex comb on midleg homolog 1 isoform 1 (SCMH1) mRNA, complete cds.//4.40E-80//149aa//63%//AF149045
 THYMU20021540
 THYMU20023560//DNA BINDING PROTEIN RFX2//6.70E-25//59aa//94%//P48378
 THYMU20024500//NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN) (NF-M)//6.20E-06//296aa//22%//P16053
 20 THYMU20025480
 THYMU20026950//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.20E-12//285aa//23%//U83176
 THYMU20028150//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1)//2.20E-33//301aa//31%//Q02246
 25 THYMU20028410//Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.//1.70E-144//345aa//81%//AF104261
 THYMU20029830
 THYMU20030460//Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA, complete cds.//2.10E-123//230aa//99%//AF279144
 30 THYMU20030690
 THYMU20031330//Homo sapiens putative nucleotide binding protein mRNA, complete cds.//1.00E-18//64aa//82%//AF118394
 THYMU20032820//ZINC FINGER PROTEIN 135//1.40E-82//258aa//55%//P52742
 35 THYMU20034400//26S proteasome subunit p44.5 [Homo sapiens]//8.80E-29//71aa//91%//AB003102
 THYMU20034790
 THYMU20036500
 THYMU20039320//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-)//1.40E-09//206aa//27%//P49695
 40 THYMU20043440
 THYMU20043560
 THYMU20044100
 THYMU20044520
 THYMU20046350
 45 THYMU20046770
 THYMU20049060//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KDA) (PR264 PROTEIN)//6.00E-41//119aa//76%//P30352
 THYMU20050010
 THYMU20051340
 50 THYMU20052460//PHORBOLIN I (FRAGMENTS)//5.80E-20//111aa//45%//P31941
 THYMU20052830//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.50E-237//477aa//90%//Y14737
 THYMU20054800
 THYMU20055450
 THYMU20055460//ESTERASE D (EC 3. 1. 1. 1)//7.60E-57//107aa//100%//P10768
 55 THYMU20055740
 THYMU20055760//Mus musculus group IIF secreted phospholipase A2 (Pla2g2f) mRNA, complete cds.//1.70E-73//165aa//75%//AF166099
 THYMU20058550

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THYMU20060480
 THYMU20062520
 THYMU20062610//DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM.//1.70E-156//585aa//50%//Q39575
 THYMU20062770//UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP).//4.20E-
 5 22//253aa//28%//P27590
 THYMU20063650//Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase, partial cds.//9.30E-57//116aa//
 97%//AJ224326
 THYMU20064680
 THYMU20066660//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//9.20E-153//
 10 361aa//85%//AF077033
 THYMU20069130
 THYMU20069460
 THYMU20069650
 THYMU20070250//TRANSETOLASE (EC 2.2.1.1) (TK).//4.50E-288//513aa//96%//P29401
 15 THYMU20071120//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.40E-229//536aa//74%//
 Q03923
 THYMU20071460
 THYMU20072580
 THYMU20073070
 20 THYMU20073080
 THYMU20077250//T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIP-
 TION FACTOR-7).//4.10E-90//176aa//96%//Q00417
 THYMU20078020
 THYMU20078240
 25 THYMU20079690
 THYMU20080490
 THYMU20081110//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//4.00E-28//60aa//
 86%//P48059
 THYMU20083390
 30 THYMU20083500
 THYMU20083830//Homo sapiens angiotensin binding protein 1 mRNA, complete cds.//2.30E-09//230aa//28%//
 AF286598
 THYMU20084520
 THYMU20086430
 35 THYMU20087270//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIB (EC 3.6.1.-).//7.20E-154//235aa//
 88%//P98195
 THYMU20089170
 THYMU20089900
 THYMU20090230//Homo sapiens ribonucleoprotein mRNA, complete cds.//9.30E-73//133aa//100%//L32610
 40 THYMU20091040
 THYMU20095920//Homo sapiens nuclear prelamin A recognition factor mRNA, complete cds.//2.90E-94//178aa//
 100%//AF128406
 THYMU20096580//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SEARS).//9.90E-20//
 45 45aa//97%//P49591
 THYMU20097920//mitogen inducible gene mig-2 - human//2.50E-197//477aa//55%//S69890
 THYMU20098350//KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) (58 KDA CYTOKERATIN).//
 3.40E-267//577aa//89%//P13647
 THYMU20099060//IG ALPHA-1 CHAIN C REGION.//1.70E-196//353aa//99%//P01876
 THYMU20100940//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IR (EC 3.6.1.-) (FRAGMENT).//0//
 50 646aa//99%//Q9Y2G3
 THYMU20104480//TRICHOHYALIN.//2.90E-21//300aa//28%//P37709
 THYMU20106990//Mus musculus evectin-2 (Evt2) mRNA, complete cds.//2.20E-112//222aa//90%//AF189817
 THYMU20110720//PROBABLE AMINOTRANSFERASE T01B1.2 (EC 2.6.1.-).//6.90E-40//211aa//41%//P91408
 THYMU20112570
 55 THYMU20112590//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//3.40E-306//534aa//
 99%//AF092094
 THYMU20115380
 THYMU20115730

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THYMU20117850
 THYMU20120240//Arabidopsis thaliana ubiquitin-specific protease (AtUBP4) mRNA, complete cds.//4.10E-18//179aa//28%//U76846
 THYMU20120730//ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (ALDH CLASS 3).//2.10E-203//379aa//99%//P30838
 5 THYMU20121040//ELONGATION FACTOR 1-DELTA (EF-1-DELTA).//5.30E-149//281aa//99%//P29692
 THYMU20128910
 THYMU20129020
 THYMU20130470
 10 THYMU20134260
 THYMU20137050
 THYMU20137570
 THYMU20139160
 THYMU20140510
 15 THYMU20143230//Homo sapiens mRNA for stabilin-1 (stab1 gene).//1.70E-177//317aa//99%//AJ275213
 THYMU20145990//nesca protein [Homo sapiens].//1.90E-152//282aa//98%//NP_055143
 THYMU20148010
 THYMU20149230
 THYMU20150190
 20 THYMU20151610//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.40E-181//344aa//100%//AF039687
 THYMU20153210//Homo sapiens Diff33 protein homolog mRNA, complete cds.//4.00E-120//404aa//54%//AF164794
 THYMU20154790
 THYMU20157620
 25 THYMU20163600
 THYMU20170080//Homo sapiens SIT protein.//9.50E-48//78aa//98%//AJ010059
 THYMU20170230//Homo sapiens sarcosine dehydrogenase (SARDH) mRNA, complete cds.//1.80E-183//260aa//99%//AF095735
 THYMU20171580
 30 THYMU20174490
 THYMU20174790
 THYMU20175260
 THYMU20176010//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.80E-20//256aa//28%//Q00808
 THYMU20177070
 35 THYMU20178440//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//2.20E-229//479aa//88%//Y14737
 THYMU20181890
 THYMU20184550
 THYMU20185470
 THYMU20185650//DIAPHANOUS PROTEIN HOMOLOG 1.//1.30E-20//85aa//44%//060610
 40 THYMU20187210
 THYMU20191970//Homo sapiens FLAMINGO 1 mRNA, partial cds.//1.80E-54//450aa//36%//AF234887
 TKIDN10000620//Homo sapiens Tax interaction protein 2 mRNA, partial cds.//1.20E-56//114aa//100%//AF028824
 TKIDN10001710
 TKIDN10001920//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//3.20E-97//226aa//73%//Q03923
 45 TRACH20011010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.30E-17//593aa//22%//P08640
 TRACH20011540//TUMOR-ASSOCIATED ANTIGEN L6.//4.70E-57//113aa//97%//P30408
 TRACH20012490
 50 TRACH20021000
 TRACH20021380//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//1.20E-276//492aa//95%//P30803
 TRACH20025370
 TRACH20026640
 55 TRACH20029880
 TRACH20040390//MATERNAL PUMILIO PROTEIN.//1.20E-177//812aa//47%//P25822
 TRACH20041090
 TRACH20043360//PUTATIVE KINESIN-LIKE PROTEIN C2F12.13.//2.30E-55//333aa//39%//014343

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TRACH20044990
 TRACH20049500
 TRACH20051590
 TRACH20057200
 5 TRACH20058000
 TRACH20073990
 TRACH20080810
 TRACH20081270
 TRACH20090060//SYNAPTOTAGMIN IV.//1.10E-12//301aa//25%/P40749
 10 TRACH20091070//ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (ALDH CLASS 3).//1.00E-173//328aa//98%/P30838
 TRACH20093400//TRICHOHYALIN.//2.30E-13//701aa//20%/P37709
 TRACH20093480
 TRACH20098510//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//1.10E-20//640aa//21%/P10587
 15 TRACH20101590
 TRACH20104510
 TRACH20108240//ribonucleoprotein - African clawed frog//4.10E-118//223aa//96%/S40774
 TRACH20113020//SELENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2).//1.80E-207//364aa//96%/Q99611
 20 TRACH20122980//HYPOTHETICAL PROTEIN MJ0798.//6.80E-13//211aa//22%/Q58208
 TRACH20123870
 TRACH20124970
 TRACH20125620
 TRACH20129180
 25 TRACH20131230//Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds.//7.50E-282//608aa//62%/AY008372
 TRACH20139280
 TRACH20140180
 TRACH20143710//RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT (EC 2.5.1.-) (RAB GERANYL-GERANYLTRANSFERASE ALPHA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE).//9.70E-07//142aa//33%/Q92696
 30 TRACH20149500//KERATIN, TYPE I CUTICULAR HA6 (HAIR KERATIN, TYPE I HA6).//1.10E-62//215aa//60%/076013
 TRACH20149720
 35 TRACH20149740//EXCITATORY AMINO ACID TRANSPORTER 5 (RETINAL GLUTAMATE TRANSPORTER).//5.00E-76//152aa//98%/000341
 TRACH20158240
 TRACH20159390
 TRACH20160800
 40 TRACH20163470//Mus musculus putative thymic stroma1 co-transporter TSCOT mRNA, complete cds.//3.20E-41//187aa//34%/AF148145
 TRACH20164100//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.40E-32//113aa//56%/P10265
 TRACH20164810
 TRACH20165330
 45 TRACH20165540//Human alpha-1 type I collagen gene surrounding osteogenesis imperfecta OI type II deletion.//4.00E-05//102aa//37%/M11162
 TRACH20167090
 TRACH20170860//IG DELTA CHAIN C REGION.//1.60E-212//383aa//100%/P01880
 TRACH20173680//Homo sapiens mRNA for LAK-4p, complete cds.//3.50E-80//410aa//38%/AB002405
 50 TRACH20174980
 TRACH20182780
 TRACH20185120
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 UTERU10001870

UTERU20000230
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 UTERU20013890
 5 UTERU20016580//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//1.90E-37//323aa//31%//Q02336
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 UTERU20031350
 10 UTERU20035770
 UTERU20040150
 UTERU20040370
 UTERU20040390
 UTERU20040730
 15 UTERU20041630//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-75//239aa//44%//Q99676
 UTERU20041970
 UTERU20045200
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 20 UTERU20064120//MYELOID UPREGULATED PROTEIN.//1.30E-79//245aa//66%//035682
 UTERU20065470
 UTERU20079240
 UTERU20083020
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 25 GLOBULIN) (PEG) (PAEG) (PLACENTAL PROTEIN 14) (PROGESTERONE-ASSOCIATED ENDOMETRIAL PRO-
 TEIN) (PROGESTAGEN-ASSOCIATED ENDOMETRIAL PROTEIN).//6.00E-73//140aa//99%//P09466
 UTERU20087070//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//4.80E-206//360aa//99%//P00736
 UTERU20087850//Homo sapiens mRNA for mucolipidin (ML4 gene).//2.70E-34//184aa//42%//AJ293970
 30 UTERU20089300
 UTERU20089390//Plectonema boryanum kinesin light chain (KLC) gene, complete cds.//3.30E-38//216aa//43%//U78597
 UTERU20089620//Homo sapiens radical fringe (RFNG) gene, partial cds.//1.50E-31//65aa//100%//AF108139
 UTERU20090940
 35 UTERU20091470
 UTERU20094830//SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM).//8.70E-09//427aa//25%//Q61079
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 UTERU20099040//ZINC TRANSPORTER 2 (ZNT-2).//9.80E-96//242aa//76%//Q62941
 40 UTERU20099510//ZINC FINGER PROTEIN 135.//2.20E-107//346aa//54%//P52742
 UTERU20141150//NUCLEAR FACTOR NF-KAPPA-B P49 SUBUNIT.//2.20E-07//76aa//47%//Q04860
 UTERU20102260
 UTERU20103040
 UTERU20103200
 45 UTERU20104310//DNA-DIRECTED RNA POLYMERASE II 14.4 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB6)
 (RPB14.4).//1.80E-48//97aa//100%//P41584
 UTERU20106510
 UTERU20121140
 UTERU20122520//MOESIN (MEMBRANE-ORGANIZING EXTENSION SPIKE PROTEIN).//6.00E-37//399aa//28%//P26042
 50 UTERU20125810
 UTERU20127030//LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ).//6.80E-175//377aa//92%//P55268
 UTERU20127150
 UTERU20128560//26.4 KDA PROTEIN IN RUVF-ASPS INTERGENIC REGION.//2.60E-17//120aa//34%//P24237
 55 UTERU20132620//AXONEME-ASSOCIATED PROTEIN MST101(2).//1.40E-15//231aa//31%//Q08696
 UTERU20134830//pellino (Drosophila) homolog 2 [Homo sapiens] //1.40E-153//361aa//729o//NP_067078
 UTERU20139760//solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kD), member 17
 [Homo sapiens]//5.40E-100//203aa//97%//XP_001136

UTERU20140010

UTERU20167570

UTERU20168960//Homo sapiens actin filament associated protein (AFAP) mRNA, complete cds.//2.60E-68//364aa//43%//AF188700

5 UTERU20169020//HOMEBOX PROSPERO-LIKE PROTEIN PROX1 (PROX 1).//1.30E-54//117aa//74%//Q91018

UTERU20173030

UTERU20176230

UTERU20177150//Homo Sapiens zinc finger protein dp mRNA, complete cds.//4.60E-10//104aa//40%//AF153201

UTERU20181270

10 UTERU20185220//Human mRNA for transcriptional activator hSNF2a, complete cds.//1.60E-125//246aa//98%//D26155

UTERU20188670//HFM1 PROTEIN.//5.10E-19//234aa//26%//P51979

UTERU20188840

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Claims

1. A polynucleotide selected from the group consisting of the following (a) to (g) :

20 (a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970;

(b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1971 to 3940;

25 (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1971 to 3940, wherein, in said amino acid sequence, one or more amino acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;

(d) a polynucleotide hybridizing to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;

30 (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970; and

35 (g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970.

2. A polypeptide encoded by the polynucleotide of claim 1, or a partial peptide thereof.

40 3. An antibody binding to the polypeptide or the peptide of claim 2.

4. A method for immunologically assaying the polypeptide or the peptide of claim 2, said method comprising the steps of contacting the polypeptide or the peptide of claim 2 with the antibody of claim 3, and observing the binding between the two.

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5. A vector comprising the polynucleotide of claim 1.

6. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5.

50 7. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5 in an expressible manner.

8. A method for producing the polypeptide or the peptide of claim 2, said method comprising the steps of culturing the transformant of claim 7 and recovering an expression product.

55 9. An oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970 or to a complementary strand thereof.

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10. Use of the oligonucleotide of claim 9 as a primer for synthesizing the polynucleotide of claim 1.

11. Use of the oligonucleotide of claim 9 as a probe for detecting the polynucleotide of claim 1.

5 12. An antisense polynucleotide against the polynucleotide of claim 1 or a part thereof.

13. A method for detecting the polynucleotide of claim 1, said method comprising the following steps of:

10 a) incubating a target polynucleotide with the oligonucleotide of claim 9 under hybridizable conditions, and
 b) detecting hybridization of the target polynucleotide with the oligonucleotide of claim 9.

14. A database of polynucleotides and/or polypeptides, said database comprising information on at least one of the
nucleotide sequences of SEQ ID NOs: 1 to 1970 and/or on at least one of the amino acid sequences of SEQ ID
NOs: 1971 to 3940.

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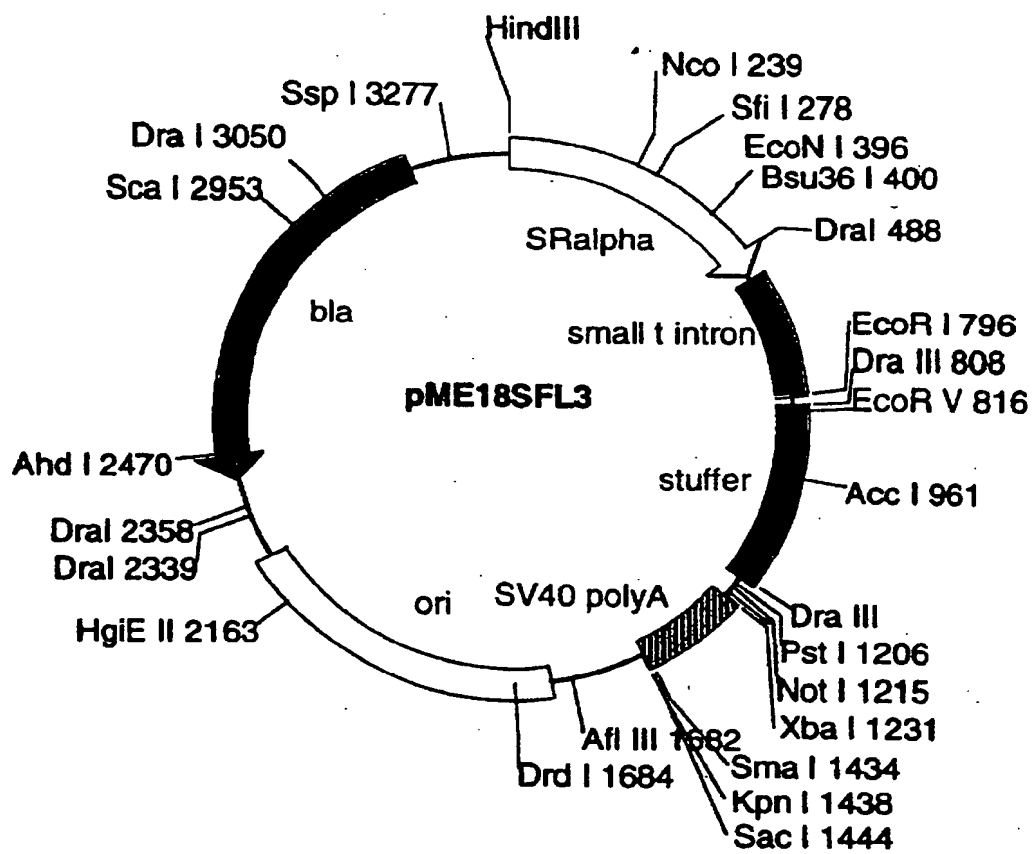
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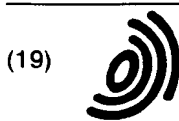
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Figure 1





(19)

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(54) **Full-length cDNA sequences**

(57) Novel full-length cDNAs are provided.
1970 cDNA derived from human have been isolated. The full-length nucleotide sequences of the cDNA and amino acid sequences encoded by the nucleotide sequences have been determined. Because the cDNA

of the present invention are full-length and contain the translation start site, they provide information useful for analyzing the functions of the polypeptide.

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EUROPEAN SEARCH REPORT

Application Number
EP 02 00 7401

DOCUMENTS CONSIDERED TO BE RELEVANT			
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The present search report has been drawn up for all claims			
Place of search BERLIN		Date of completion of the search 4 February 2003	Examiner De Kok, A
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

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Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)	
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X	<p>& WO 01 04286 A</p> <p>18 January 2001 (2001-01-18)</p> <p>-----</p>	1		
<p>The present search report has been drawn up for all claims</p>				
Place of search		Date of completion of the search	Examiner	
BERLIN		4 February 2003	De Kok, A	
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone</p> <p>Y : particularly relevant if combined with another document of the same category</p> <p>A : technological background</p> <p>O : non-written disclosure</p> <p>P : intermediate document</p> <p>T : theory or principle underlying the invention</p> <p>E : earlier patent document, but published on, or after the filing date</p> <p>D : document cited in the application</p> <p>L : document cited for other reasons</p> <p>& : member of the same patent family, corresponding document</p>				

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CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

- ☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):
- ☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

- ☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.
- ☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.
- ☐ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:
- ☒ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

1-14, all partially



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LACK OF UNITY OF INVENTION
SHEET B

Application Number

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The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Invention 1: claims 1-14, all partially

A polynucleotide comprising a nucleic acid having the sequence defined by Seq.Id.No.1 and the polypeptide comprising Seq.Id.No.1971 encoded by said polynucleotide and uses thereof as defined by claims 3-14.

Inventions 2-1970: claims 1-14, all partially

As invention 1, but limited to each single polynucleotide having a Seq.Id. in the order as listed in claim 1, starting with Seq.Id.No.2 (and the corresponding polypeptide having Seq.Id.No. 1971) and ending with Seq.Id.No. 1970 (and the corresponding polypeptide having Seq.Id.No. 3940).

For the sake of conciseness, the subject-matter of the first invention is explicitly defined, the subject-matter of the other inventions is defined by analogy thereto.

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 02 00 7401

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
The members are as contained in the European Patent Office EDP file on
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04-02-2003

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For more details about this annex : see Official Journal of the European Patent Office, No. 12/82